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;           REFERENCE/DOCKET NUMBER: 28111/34800
;   INFORMATION FOR SEQ ID NO: 8:
;       SEQUENCE CHARACTERISTICS:
;           LENGTH: 32 amino acids
;           TYPE: amino acid
;           TOPOLOGY: linear
;       SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-767-395-8

  Query Match           89.7%;  Score 26;  DB 10;  Length 32;
  Best Local Similarity  80.0%;  Pred. No. 19;
  Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 SYTMH 5
          |||:|
Db      9 SYTLH 13


RESULT 2
US     083-357-712
;      ence 712, Application US/10083357
; Publication No. US20030054370A1
; GENERAL INFORMATION:
;  APPLICANT: Qiandong Zeng et al.
;  TITLE OF INVENTION: Systemic Discovery of New Genes
;  FILE REFERENCE: 032796-090
;  CURRENT APPLICATION NUMBER: US/10/083,357
;  CURRENT FILING DATE:  2002-02-27
;  NUMBER OF SEQ ID NOS: 1346
; SEQ ID NO 712
;    LENGTH: 82
;    TYPE: PRT
;    ORGANISM: Saccharomyces cerevisiae
US-10-083-357-712

  Query Match           89.7%;  Score 26;  DB 9;  Length 82;
  Best Local Similarity  80.0%;  Pred. No. 47;
  Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 SYTMH 5
          :||||
Db      1 NYTMH 5


RESULT 3
US-09-903-456-20
; Sequence 20, Application US/09903456
;      nt No. US20020138874A1
;      RAL INFORMATION:
;  APPLICANT: Abbott Laboratories
;  APPLICANT:  Mukerji, Pradip
;  APPLICANT:  Leonard, Amanda Eun-Yeong
;  APPLICANT:  Huang, Yung-Sheng
;  APPLICANT:  Pereira, Suzette L.
;  TITLE OF INVENTION: ELONGASE GENES AND USES THEREOF
;  FILE REFERENCE: 6407.US.P3
;  CURRENT APPLICATION NUMBER: US/09/903,456
;  CURRENT FILING DATE:  2001-07-11
;  PRIOR APPLICATION NUMBER: US 09/624,670
;  PRIOR FILING DATE: 2000-07-24
;  PRIOR APPLICATION NUMBER: US 09/379,095
;  PRIOR FILING DATE: 1999-08-23
;  PRIOR APPLICATION NUMBER: US 09/145,828
;  PRIOR FILING DATE: 1998-09-02
;  NUMBER OF SEQ ID NOS: 116
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 20
;    LENGTH: 238
;    TYPE: PRT
;    ORGANISM: Caenorhabditis elegans
US-09-903-456-20

  Query Match           89.7%;  Score 26;  DB 10;  Length 238;
  Best Local Similarity  80.0%;  Pred. No. 1.3e+02;
  Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 SYTMH 5
          |||:|
Db    232 SYTLH 236


RESULT 4
US-10-043-487-407
; Sequence 407, Application US/10043487
; Publication No. US20030055220A1
; GENERAL INFORMATION:
;  APPLICANT: HYBRIGENICS
;  APPLICANT:  Pierre, LEGRAIN
;  TITLE OF INVENTION: Protein-protein interactions between Shigella Flexneri polypeptid
;  TITLE OF INVENTION:  mammalian polypeptides
;  FILE REFERENCE: B4778A
;  CURRENT APPLICATION NUMBER: US/10/043,487
;  CURRENT FILING DATE:  2002-04-30
;  PRIOR APPLICATION NUMBER: US 60/261,130
;  PRIOR FILING DATE: 2001-01-12
;  NUMBER OF SEQ ID NOS: 561
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 407
;    LENGTH: 335
;    TYPE: PRT
;    ORGANISM: Shigella Flexneri
US-10-043-487-407

  Query Match           89.7%;  Score 26;  DB 9;  Length 335;
  Best Local Similarity  80.0%;  Pred. No. 1.9e+02;
  Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 SYTMH 5
          |||:|
Db    119 SYTLH 123


RESULT 5
US-09-925-301-984
; Sequence 984, Application US/09925301
; Patent No. US20020052308A1
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al.
;  TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
;  FILE REFERENCE: PA106
;  CURRENT APPLICATION NUMBER: US/09/925,301
;  CURRENT FILING DATE:  2001-08-10
;  PRIOR APPLICATION NUMBER: PCT/US00/05882
;  PRIOR FILING DATE: 2000-03-08
;  PRIOR APPLICATION NUMBER: 60/124,270
;  PRIOR FILING DATE: 1999-03-12
;  NUMBER OF SEQ ID NOS: 1694
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 984
;    LENGTH: 402
;    TYPE: PRT
;    ORGANISM: Homo sapiens
US-09-925-301-984

  Query Match           89.7%;  Score 26;  DB 10;  Length 402;
  Best Local Similarity  80.0%;  Pred. No. 2.3e+02;
  Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 SYTMH 5
          |||:|
Db    116 SYTLH 120


RESULT 6
US-09-742-580-8
; Sequence 8, Application US/09742580
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GenCore version 5.1.4_p5_4578

OM protein - protein search, using sw model

Run on: April 16, 2003, 17:21:54 ; Search time 1.47368 Seconds
(without alignments)
256.547 Million cell updates/sec

Title: US-09-644-668A-27
Perfect score: 29
Sequence: 1 SYTMH 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 288829 seqs, 75613885 residues

Total number of hits satisfying chosen parameters: 288829

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
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3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	26	89.7	32	10	US-09-767-395-8	Sequence 8, Appli
2	26	89.7	82	9	US-10-083-357-712	Sequence 712, App
3	26	89.7	238	10	US-09-903-456-20	Sequence 20, Appl
4	26	89.7	335	9	US-10-043-487-407	Sequence 407, App
5	26	89.7	402	10	US-09-925-301-984	Sequence 984, App
6	26	89.7	505	9	US-09-742-580-8	Sequence 8, Appli
7	26	89.7	505	9	US-09-742-581-8	Sequence 8, Appli
8	26	89.7	505	10	US-09-742-582-8	Sequence 8, Appli
9	26	89.7	836	10	US-09-953-688A-7	Sequence 7, Appli
10	25	86.2	86	10	US-09-864-761-39492	Sequence 39492, A
11	25	86.2	99	9	US-10-194-975-27	Sequence 27, Appl
12	25	86.2	117	9	US-09-956-206A-76	Sequence 76, Appl
13	25	86.2	117	9	US-09-956-206A-78	Sequence 78, Appl
14	25	86.2	119	9	US-09-813-398-2	Sequence 2, Appli
15	25	86.2	119	9	US-09-795-515-11	Sequence 11, Appl
16	25	86.2	119	9	US-09-795-515-12	Sequence 12, Appl
17	25	86.2	119	9	US-09-795-515-13	Sequence 13, Appl
18	25	86.2	119	9	US-09-795-515-14	Sequence 14, Appl
19	25	86.2	119	9	US-09-795-515-15	Sequence 15, Appl
20	25	86.2	119	9	US-09-795-515-16	Sequence 16, Appl
21	25	86.2	119	9	US-09-795-515-17	Sequence 17, Appl
22	25	86.2	119	9	US-09-795-515-18	Sequence 18, Appl
23	25	86.2	119	9	US-09-795-515-19	Sequence 19, Appl
24	25	86.2	119	9	US-09-795-515-20	Sequence 20, Appl
25	25	86.2	119	9	US-09-795-515-21	Sequence 21, Appl
26	25	86.2	119	9	US-09-795-515-22	Sequence 22, Appl
27	25	86.2	119	9	US-09-795-515-23	Sequence 23, Appl
28	25	86.2	119	9	US-09-795-515-24	Sequence 24, Appl
29	25	86.2	119	9	US-09-795-515-30	Sequence 30, Appl
30	25	86.2	127	9	US-09-848-798-27	Sequence 27, Appl
31	25	86.2	131	9	US-09-848-798-28	Sequence 28, Appl
32	25	86.2	136	9	US-09-956-206A-47	Sequence 47, Appl
33	25	86.2	136	9	US-09-956-206A-63	Sequence 63, Appl
34	25	86.2	138	12	US-10-066-895-6	Sequence 6, Appli
35	25	86.2	138	12	US-10-066-895-7	Sequence 7, Appli
36	25	86.2	138	12	US-10-066-895-8	Sequence 8, Appli
37	25	86.2	139	12	US-10-066-895-5	Sequence 5, Appli
38	25	86.2	169	10	US-09-867-550-682	Sequence 682, App
39	25	86.2	209	10	US-09-393-634-13	Sequence 13, Appl
40	25	86.2	232	10	US-09-754-998-2	Sequence 2, Appli
41	25	86.2	232	10	US-09-864-761-33560	Sequence 33560, A
42	25	86.2	232	10	US-09-864-761-34077	Sequence 34077, A
43	25	86.2	232	10	US-09-811-384-10	Sequence 10, Appl
44	25	86.2	241	10	US-09-940-166A-1	Sequence 1, Appli
45	25	86.2	247	9	US-09-880-748-1307	Sequence 1307, Ap

ALIGNMENTS

```
RESULT 1
US-09-767-395-8
; Sequence 8, Application US/09767395
; Patent No. US20020004215A1
;  GENERAL INFORMATION:
;       APPLICANT: Osbourn, Jane K
;                  Derbyshire, Elaine J
;                  McCafferty, John G
;                  Vaughan, Tristan J
;                  Johnson, Kevin S
;       TITLE OF INVENTION: Labelling and selection of molecules
;       NUMBER OF SEQUENCES: 36
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
;            STREET: 6300 Sears Tower, 233 South Wacker Drive
;            CITY: Chicago
;            STATE: Illinois
;            COUNTRY: USA
;            ZIP: 60606-6402
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/767,395
;            FILING DATE: 23-Jan-2001
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 09/098,244
;            FILING DATE: <Unknown>
;            APPLICATION NUMBER: PCT/GB97/01835
;            FILING DATE: 08-JUL-1997
;            APPLICATION NUMBER: GB 9614292.2
;            FILING DATE: 08-JUL-1996
;            APPLICATION NUMBER: GB 9624880.2
;            FILING DATE: 29-NOV-1996
;            APPLICATION NUMBER: GB 9712818.5
;            FILING DATE: 18-JUN-1997
;       ATTORNEY/AGENT INFORMATION:
;            NAME: David W. Clough
;            REGISTRATION NUMBER: 36,107
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RT   divergence in early regulation and replication regions.";
RL   DNA Res. 6:235-240(1999).
RN   [5]
RP   SEQUENCE FROM N.A.
RC   SPECIES=Stx2 converting bacteriophage I; STRAIN=STX2 PHAGE-I;
RA   Sato T., Shimizu T., Watarai M., Kobayashi M., Kano S., Hamabata T.,
RA   Yamasaki S., Takeda Y.;
RT   "Genomic sequence of Shiga toxin 2-converting phage isolated from
RT   Escherichia coli O157:H7 Okayama strain and comparison with other
RT   Shiga toxin 2-converting phages.";
RL   Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF125520; AAD25413.1; -.
DR   EMBL; AP000363; BAA84290.1; -.
DR   EMBL; AP004402; BAB87939.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   95 AA;  10446 MW;  5F2FB7C449685BAC CRC64;

  Query Match           100.0%;  Score 29;  DB 9;  Length 95;
  Best Local Similarity  100.0%;  Pred. No. 9.6;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 SYTMH 5
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Db      30 SYTMH 34


RESULT 2
Q9KXG9
ID   Q9KXG9      PRELIMINARY;      PRT;    95 AA.
AC   Q9KXG9;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Hypothetical protein H0078.
GN   H0078 OR ECS1167.
OS   Escherichia coli O157:H7.
OC   Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC   Escherichia.
OX   NCBI_TaxID=83334;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=O157:H7;
RX   MEDLINE=20198780; PubMed=10734605;
RA   Makino K., Yokoyama K., Kubota Y., Yutsudo C.H., Kimura S.,
RA   Kurokawa K., Ishii K., Hattori M., Tatsuno I., Abe H., Iida T.,
RA   Yamamoto K., Ohnishi M., Hayashi T., Yasunaga T., Honda T.,
RA   Sasakawa C., Shinagawa H.;
RT   "Complete nucleotide sequence of the prophage VT2-Sakai carrying the
RT   verotoxin 2 genes of the enterohemorrhagic Escherichia coli O157:H7
RT   derived from the Sakai outbreak.";
RL   Genes Genet. Syst. 74:227-239(1999).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=O157:H7 / RIMD 0509952;
RX   MEDLINE=21156231; PubMed=11258796;
RA   Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA   Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA   Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
RA   Kuhara S., Shiba T., Hattori M., Shinagawa H.;
RT   "Complete genome sequence of enterohemorrhagic Escherichia coli
RT   O157:H7 and genomic comparison with a laboratory strain K-12.";
RL   DNA Res. 8:11-22(2001).
DR   EMBL; AP000422; BAA94106.1; -.
DR   EMBL; AP002554; BAB34590.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   95 AA;  10446 MW;  5F2FB7C449685BAC CRC64;

  Query Match           100.0%;  Score 29;  DB 16;  Length 95;
  Best Local Similarity  100.0%;  Pred. No. 9.6;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 SYTMH 5
           |||||
Db      30 SYTMH 34


RESULT 3
Q95TC7
ID   Q95TC7      PRELIMINARY;      PRT;   123 AA.
AC   Q95TC7;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   GH01923p.
GN   CG6783.
OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC   Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7227;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BERKELEY;
RA   Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA   Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
RA   Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
RA   Nunoo J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K.,
RA   Yu C., Lewis S.E., Rubin G.M., Celniker S.;
RL   Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY060229; AAL25268.1; -.
DR   FlyBase; FBgn0037913; CG6783.
SQ   SEQUENCE   123 AA;  14109 MW;  838C453CEE4CEB7F CRC64;

  Query Match           100.0%;  Score 29;  DB 5;  Length 123;
  Best Local Similarity  100.0%;  Pred. No. 13;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 SYTMH 5
           |||||
Db      95 SYTMH 99


RESULT 4
O96687
ID   O96687      PRELIMINARY;      PRT;   242 AA.
AC   O96687;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Fibrinolytic enzyme (Fragment).
OS   Lumbricus bimastus.
OC   Eukaryota; Metazoa; Annelida; Clitellata; Oligochaeta; Haplotaxida;
OC   Lumbricina; Lumbricidae; Lumbricus.
OX   NCBI_TaxID=86417;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Liang G., Meng X., Fu S., Li L., Hou Y., Chen F., Shan F., Qin Y.;
RT   "Cloning of the genes encoding fibrinolytic enzymes from Lumbricus
RT   bimastus.";
RL   Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC       TRYPSIN FAMILY.
DR   EMBL; AF109648; AAD05563.1; -.
DR   HSSP; P20231; 1AAO.
DR   InterPro; IPR001314; Chymotrypsin.
DR   InterPro; IPR001254; Ser_protease_Try.
DR   Pfam; PF00089; trypsin; 1.
DR   PRINTS; PR00722; CHYMOTRYPSIN.
DR   SMART; SM00020; Tryp_SPc; 1.
DR   PROSITE; PS50240; TRYPSIN_DOM; 1.
DR   PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR   PROSITE; PS00135; TRYPSIN_SER; 1.
KW   Hydrolase; Serine protease.
FT   NON_TER       1       1
SQ   SEQUENCE   242 AA;  24837 MW;  F912425D2724745D CRC64;
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GenCore version 5.1.4_p5_4578

OM protein - protein search, using sw model

Run on: April 16, 2003, 17:13:59 ; Search time 5.12281 Seconds
(without alignments)
201.108 Million cell updates/sec

Title: US-09-644-668A-27
Perfect score: 29
Sequence: 1 SYTMH 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

To number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_21:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	29	100.0	95	9	Q9XJH3	Q9xjh3 bacteriopha
2	29	100.0	95	16	Q9KXG9	Q9kxg9 escherichia
3	29	100.0	123	5	Q95TC7	Q95tc7 drosophila
4	29	100.0	242	5	O96687	O96687 lumbricus b
5	29	100.0	388	17	Q8TI30	Q8ti30 methanosarc
6	29	100.0	945	5	Q93378	Q93378 caenorhabdi
7	26	89.7	56	2	Q52223	Q52223 leuconostoc
8	26	89.7	94	17	Q9HKT2	Q9hkt2 thermoplasm
9	26	89.7	113	2	Q93I89	Q93i89 staphylococ
10	26	89.7	121	4	Q9UMI0	Q9umi0 homo sapien
11	26	89.7	132	4	Q9UG94	Q9ug94 homo sapien
12	26	89.7	143	4	Q9UNE4	Q9une4 homo sapien
13	26	89.7	143	4	Q16502	Q16502 homo sapien
14	26	89.7	144	4	Q13830	Q13830 homo sapien
15	26	89.7	157	1	P94805	P94805 haloferax s
16	26	89.7	158	4	Q15229	Q15229 homo sapien
17	26	89.7	171	10	Q9ATP4	Q9atp4 pennisetum
18	26	89.7	178	10	Q9XF17	Q9xf17 rosa hybrid
19	26	89.7	178	17	Q9UYP4	Q9uyp4 pyrococcus
20	26	89.7	190	8	Q9B3V2	Q9b3v2 plethodon g
21	26	89.7	190	8	Q9B3U4	Q9b3u4 plethodon t
22	26	89.7	192	8	Q9B3U8	Q9b3u8 plethodon p
23	26	89.7	200	8	Q9B3U3	Q9b3u3 plethodon y
24	26	89.7	203	8	Q9B3V3	Q9b3v3 plethodon f
25	26	89.7	213	16	Q8XZD7	Q8xzd7 ralstonia s
26	26	89.7	216	12	Q69574	Q69574 human herpe
27	26	89.7	218	8	Q9B3U2	Q9b3u2 plethodon w
28	26	89.7	220	8	Q9B3U9	Q9b3u9 plethodon o
29	26	89.7	231	8	O79474	O79474 pelamis pla
30	26	89.7	231	8	Q8WA07	Q8wa07 demansia at
31	26	89.7	231	8	Q8WA04	Q8wa04 homoroselap
32	26	89.7	231	8	Q8WA03	Q8wa03 laticauda c
33	26	89.7	231	8	Q8WA00	Q8wa00 notechis at
34	26	89.7	236	4	Q9UEA4	Q9uea4 homo sapien
35	26	89.7	248	16	Q9X866	Q9x866 streptomyce
36	26	89.7	281	5	Q20904	Q20904 caenorhabdi
37	26	89.7	306	11	Q99KR1	Q99kr1 mus musculu
38	26	89.7	318	16	O51270	O51270 borrelia bu
39	26	89.7	319	16	Q8XY04	Q8xy04 ralstonia s
40	26	89.7	324	4	Q9UPK9	Q9upk9 homo sapien
41	26	89.7	326	4	Q9UPK8	Q9upk8 homo sapien
42	26	89.7	326	4	Q13048	Q13048 homo sapien
43	26	89.7	332	4	Q15242	Q15242 homo sapien
44	26	89.7	333	4	O75238	O75238 homo sapien
45	26	89.7	335	4	Q15239	Q15239 homo sapien

ALIGNMENTS

RESULT 1
Q9XJH3
ID Q9XJH3 PRELIMINARY; PRT; 95 AA.
AC Q9XJH3;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical 10.4 kDa protein.
GN L0068.
OS Bacteriophage 933W,
OS Bacteriophage VT2-Sa, and
OS Stx2 converting bacteriophage I.
OC Viruses; dsDNA viruses, no RNA stage; unclassified dsDNA phages.
OX NCBI_TaxID=10730, 97081, 180816;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=Phage 933W;
RX MEDLINE=99173898; PubMed=10074068;
RA Plunkett G. III, Rose D.J., Durfee T.J., Blattner F.R.;
RT "Sequence of Shiga toxin 2 phage 933W from Escherichia coli O157:H7:
RT Shiga toxin as a phage late-gene product.";
RL J. Bacteriol. 181:1767-1778(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=Phage 933W;
RA Plunkett G. III;
RL Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=Phage VT2-Sa;
RA Miyamoto H.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC SPECIES=Phage VT2-Sa;
RX MEDLINE=99419919; PubMed=10492170;
RA Miyamoto H., Nakai W., Yajima N., Fujibayashi A., Higuchi T., Sato K.,
RA Matsushiro A.;
RT "Sequence analysis of Stx2-Converting phage VT2-Sa shows a great

```
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Frangsmyr L., Teglund S., Israelsson A., Hammarstrom S.;
RT   "Characterization of upstream promotor region, exon1 and exon2 of the
RT   PSG gene family.";
RL   Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: Secreted (Potential).
CC   -!- DEVELOPMENTAL STAGE: PSBG ARE PRODUCED IN HIGH QUANTITY DURING
CC       PREGNANCY.
CC   -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CEA
CC       SUBFAMILY.
CC   -!- SIMILARITY: CONTAINS 3 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC   -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF106562; AAD21024.1; -.
DR   EMBL; AF106561; AAD21024.1; JOINED.
DR   MIM; 176401; -.
KW   Immunoglobulin domain; Glycoprotein; Signal; Multigene family.
FT   SIGNAL        1     34       POTENTIAL.
FT   CHAIN        35   >143       PREGNANCY-SPECIFIC BETA-1-GLYCOPROTEIN
FT                                13.
FT   DOMAIN       35   >143       IG-LIKE V-TYPE DOMAIN.
FT   SITE        127    129       CELL ATTACHMENT SITE (POTENTIAL).
FT   CARBOHYD     61     61       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    104    104       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    111    111       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   NON_TER     143    143
SQ   SEQUENCE   143 AA;  16065 MW;  2C452383C8381D28 CRC64;

  Query Match             89.7%;  Score 26;  DB 1;  Length 143;
  Best Local Similarity   80.0%;  Pred. No. 19;
  Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 SYTMH 5
           |||:|
Db     119 SYTLH 123


RESULT 3
PSG8_HUMAN
ID   PSG8_HUMAN      STANDARD;      PRT;   144 AA.
AC   Q9UQ74;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Pregnancy-specific beta-1-glycoprotein 8 precursor (PSBG-8)
DE   (Fragment).
GN   PSG8.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Frangsmyr L., Teglund S., Israelsson A., Hammarstrom S.;
RT   "Characterization of upstream promotor region, exon1 and exon2 of the
RT   PSG gene family.";
RL   Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: Secreted (Potential).
CC   -!- DEVELOPMENTAL STAGE: PSBG ARE PRODUCED IN HIGH QUANTITY DURING
CC       PREGNANCY.
CC   -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CEA
CC       SUBFAMILY.
CC   -!- SIMILARITY: CONTAINS 3 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC   -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF106556; AAD21022.1; -.
DR   EMBL; AF106555; AAD21022.1; JOINED.
DR   Genew; HGNC:9525; PSG8.
DR   MIM; 176397; -.
KW   Immunoglobulin domain; Glycoprotein; Signal; Repeat; Multigene family.
FT   SIGNAL        1     34       POTENTIAL.
FT   CHAIN        35   >144       PREGNANCY-SPECIFIC BETA-1-GLYCOPROTEIN 8.
FT   DOMAIN       35    144       IG-LIKE V-TYPE DOMAIN.
FT   CARBOHYD     61     61       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    104    104       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    111    111       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   NON_TER     144    144
SQ   SEQUENCE   144 AA;  16109 MW;  0A83A6711042C1FE CRC64;

  Query Match             89.7%;  Score 26;  DB 1;  Length 144;
  Best Local Similarity   80.0%;  Pred. No. 19;
  Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 SYTMH 5
           |||:|
Db     119 SYTLH 123


RESULT 4
SC1_OCTVU
ID   SC1_OCTVU      STANDARD;      PRT;   214 AA.
AC   P27013;
DT   01-AUG-1992 (Rel. 23, Created)
DT   01-AUG-1992 (Rel. 23, Last sequence update)
DT   01-NOV-1997 (Rel. 35, Last annotation update)
DE   S-crystallin 1.
GN   OCTS1.
OS   Octopus vulgaris (Octopus).
OC   Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Octopoda;
OC   Incirrata; Octopodidae; Octopus.
OX   NCBI_TaxID=6645;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lens;
RX   MEDLINE=92328840; PubMed=1627174;
RA   Lin C.-W., Chiou S.-H.;
RT   "Facile cloning and sequencing of S-crystallin genes from octopus
RT   lenses based on polymerase chain reaction.";
RL   Biochem. Int. 27:173-178(1992).
CC   -!- FUNCTION: S-CRYSTALLINS ARE STRUCTURAL COMPONENTS OF SQUIDS AND
CC       OCTOPI EYE LENS. CONTAINS RELATIVELY LITTLE GST ACTIVITY (1/1000
CC       OF THAT OF MAMMALIAN GST ENZYME).
CC   -!- TISSUE SPECIFICITY: LENS.
CC   -!- SIMILARITY: BELONGS TO THE GST SUPERFAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X65543; CAA46511.1; -.
DR   PIR; S21340; S21340.
DR   HSSP; P46088; 2GSQ.
```

GenCore version 5.1.4_p5_4578

OM protein - protein search, using sw model

Run on: April 16, 2003, 16:57:42 ; Search time 0.982456 Seconds
(without alignments)
211.085 Million cell updates/sec

Title: US-09-644-668A-27
Perfect score: 29
Sequence: 1 SYTMH 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	26	89.7	102	1	YM88_YEAST	Q04838 saccharomyc
2	26	89.7	143	1	PSGD_HUMAN	Q9uq72 homo sapien
3	26	89.7	144	1	PSG8_HUMAN	Q9uq74 homo sapien
4	26	89.7	214	1	SC1_OCTVU	P27013 octopus vul
5	26	89.7	215	1	SC2_OCTVU	P27014 octopus vul
6	26	89.7	215	1	SC3_OCTDO	P27011 octopus dof
7	26	89.7	215	1	SC3_OCTVU	Q25626 octopus vul
8	26	89.7	215	1	SC4_OCTDO	P27012 octopus dof
9	26	89.7	282	1	LPXC_CHLPN	Q9z7q2 chlamydia p
10	26	89.7	286	1	LPXC_CHLMU	Q9pjk9 chlamydia m
11	26	89.7	286	1	LPXC_CHLTR	O84538 chlamydia t
12	26	89.7	315	1	ISPE_SYNY3	P72663 synechocyst
13	26	89.7	323	1	ARG1_SCHPO	P37818 schizosacch
14	26	89.7	323	1	ARG2_SCHPO	Q10066 schizosacch
15	26	89.7	335	1	PSG2_HUMAN	P11465 homo sapien
16	26	89.7	335	1	PSG5_HUMAN	Q15238 homo sapien
17	26	89.7	389	1	PRS8_DICDI	P34124 dictyosteli
18	26	89.7	402	1	PRS8_MANSE	P54814 manduca sex
19	26	89.7	405	1	PRS8_DROME	O18413 drosophila
20	26	89.7	406	1	PRS8_HUMAN	P47210 homo sapien
21	26	89.7	419	1	PSG1_HUMAN	P11464 homo sapien
22	26	89.7	419	1	PSG4_HUMAN	Q00888 homo sapien
23	26	89.7	419	1	PSG7_HUMAN	Q13046 homo sapien
24	26	89.7	424	1	PSGA_HUMAN	Q15235 homo sapien
25	26	89.7	424	1	PSGC_HUMAN	O75244 homo sapien
26	26	89.7	428	1	PSG3_HUMAN	Q16557 homo sapien
27	26	89.7	435	1	PSG6_HUMAN	Q00889 homo sapien
28	26	89.7	461	1	PRS8_XENLA	P46470 xenopus lae
29	26	89.7	462	1	HMCS_CAEEL	P54871 caenorhabdi
30	26	89.7	736	1	ETR2_LYCES	O49187 lycopersico
31	26	89.7	740	1	ETR1_CUCMR	O82436 cucumis mel
32	26	89.7	740	1	ETR1_CUCSA	Q9ssy6 cucumis sat
33	26	89.7	1748	1	POLR_ELV	P35928 erysimum la
34	26	89.7	3063	1	CA1C_HUMAN	Q99715 homo sapien
35	26	89.7	3119	1	CA1C_MOUSE	Q60847 mus musculu
36	26	89.7	3124	1	CA1C_CHICK	P13944 gallus gall
37	25	86.2	138	1	TSHB_CANFA	P54828 canis famil
38	25	86.2	138	1	TSHB_HUMAN	P01222 homo sapien
39	25	86.2	185	1	YAIS_ECOLI	P71311 escherichia
40	25	86.2	219	1	HIS8_MYCSM	P28735 mycobacteri
41	25	86.2	272	1	YEGX_ECOLI	P76421 escherichia
42	25	86.2	296	1	ARGI_BACSU	P39138 bacillus su
43	25	86.2	297	1	Y060_MYCGE	P47306 mycoplasma
44	25	86.2	299	1	ARGI_BACCD	P53608 bacillus ca
45	25	86.2	309	1	YEEY_ECOLI	P76369 escherichia

ALIGNMENTS

RESULT 1
YM88_YEAST
ID YM88_YEAST STANDARD; PRT; 102 AA.
AC Q04838;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Very hypothetical 11.8 kDa protein in HOR7-COX7 intergenic region.
GN YMR254C OR YM9920.08C.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288c / AB972;
RA Hunt S., Bowman S., Barrell B.G., Rajandream M.A., Walsh S.V.;
RL Submitted (MAR-1995) to the EMBL/GenBank/DDBJ databases.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC ---
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CC ---
DR EMBL; Z48639; CAA88581.1; -.
DR SGD; S0004867; YMR254C.
KW Hypothetical protein; Transmembrane.
FT TRANSMEM 1 21 POTENTIAL.
FT TRANSMEM 42 62 POTENTIAL.
FT TRANSMEM 68 88 POTENTIAL.
SQ SEQUENCE 102 AA; 11816 MW; 7AF028226F33964D CRC64;

Query Match 89.7%; Score 26; DB 1; Length 102;
Best Local Similarity 80.0%; Pred. No. 13;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
Qy       1 SYTMH 5
             :||||
Db      47 TYTMH 51
```

RESULT 2
PSGD_HUMAN
ID PSGD_HUMAN STANDARD; PRT; 143 AA.
AC Q9UQ72;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Pregnancy-specific beta-1-glycoprotein 13 precursor (PSBG-13)
DE (Fragment).
GN PSG13.
OS Homo sapiens (Human).

A;Pathway: detoxification
A;Note: this protein has weak catalytic activity
C;Superfamily: glutathione transferase
C;Keywords: detoxification; glutathione; transferase

  Query Match 89.7%; Score 26; DB 2; Length 214;
  Best Local Similarity 80.0%; Pred. No. 89;
  Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYTMH 5
 |||:|
Db 3 SYTLH 7

RESULT 13
S56762
S-crystallin isoform S3 - common octopus
C;Species: Octopus vulgaris (common octopus)
C;Date: 10-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 18-Jun-1999
C;Accession: S56762; S37148
R;Ju, S.H.; Yu, C.W.; Lin, C.W.; Pan, F.M.; Lu, S.F.; Lee, H.J.; Chang, G.G.
Biochem. J. 309, 793-800, 1995
A;Title: Octopus S-crystallins with endogenous glutathione S-transferase (GST) activity:
A;Reference number: S56760; MUID:95366954; PMID:7639695
A;Accession: S56762
A;Molecule type: mRNA
A;Residues: 1-215 <CHI>
A;Cross-references: EMBL:X74858; NID:g400475; PIDN:CAA52850.1; PID:g400476
C;Superfamily: glutathione transferase

  Query Match 89.7%; Score 26; DB 2; Length 215;
  Best Local Similarity 80.0%; Pred. No. 89;
  Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYTMH 5
 |||:|
Db 3 SYTLH 7

RESULT 14
D41681
S-crystallin 4 - giant octopus
C;Species: Octopus dofleini (giant octopus)
C;Date: 30-Jun-1992 #sequence_revision 18-Sep-1992 #text_change 18-Jun-1999
C;Accession: D41681
R;Tomarev, S.I.; Zinovieva, R.D.; Piatigorsky, J.
J. Biol. Chem. 266, 24226-24231, 1991
A;Title: Crystallins of the octopus lens. Recruitment from detoxification enzymes.
A;Reference number: A41681; MUID:92084735; PMID:1721068
A;Accession: D41681
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-215 <TOM>
A;Cross-references: GB:M65187; NID:g159734; PIDN:AAA29389.1; PID:g159735
C;Superfamily: glutathione transferase

  Query Match 89.7%; Score 26; DB 2; Length 215;
  Best Local Similarity 80.0%; Pred. No. 89;
  Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYTMH 5
 |||:|
Db 3 SYTLH 7

RESULT 15
C41681
S-crystallin 3 - giant octopus
C;Species: Octopus dofleini (giant octopus)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 18-Jun-1999
C;Accession: C41681
R;Tomarev, S.I.; Zinovieva, R.D.; Piatigorsky, J.
J. Biol. Chem. 266, 24226-24231, 1991
A;Title: Crystallins of the octopus lens. Recruitment from detoxification enzymes.
A;Reference number: A41681; MUID:92084735; PMID:1721068
A;Accession: C41681
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-215 <TOM>
A;Cross-references: GB:M65186; NID:g159732; PIDN:AAA29388.1; PID:g159733
C;Superfamily: glutathione transferase

  Query Match 89.7%; Score 26; DB 2; Length 215;
  Best Local Similarity 80.0%; Pred. No. 89;
  Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYTMH 5
 |||:|
Db 3 SYTLH 7

Search completed: April 16, 2003, 17:21:37
Job time : 2.54386 secs

OM protein - protein search, using sw model

Run on: April 16, 2003, 17:11:36 ; Search time 1.54386 Seconds
(without alignments)
311.344 Million cell updates/sec

Title: US-09-644-668A-27
Perfect score: 29
Sequence: 1 SYTMH 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	29	100.0	95	2	G90774	hypothetical prote
2	29	100.0	96	2	S17230	Ig heavy chain V r
3	29	100.0	96	2	S17621	Ig heavy chain V r
4	29	100.0	96	2	S17620	Ig heavy chain V r
5	29	100.0	102	2	S26471	Ig heavy chain V r
6	29	100.0	945	2	T19943	hypothetical prote
7	26	89.7	102	2	S53076	probable membrane
8	26	89.7	113	2	E33936	Ig heavy chain V r
9	26	89.7	121	2	D32268	carcinoembryonic a
10	26	89.7	157	2	T44794	hypothetical prote
11	26	89.7	178	2	C75059	hypothetical prote
12	26	89.7	214	2	S56758	S-crystallin isofo
13	26	89.7	215	2	S56762	S-crystallin isofo
14	26	89.7	215	2	D41681	S-crystallin 4 - g
15	26	89.7	215	2	C41681	S-crystallin 3 - g
16	26	89.7	215	2	S56759	S-crystallin isofo
17	26	89.7	248	2	T36093	probable DNA methy
18	26	89.7	281	2	T22791	hypothetical prote
19	26	89.7	282	2	A86572	myristoyl GlcNac d
20	26	89.7	282	2	E72051	UDP-3-O-[3-hydroxy
21	26	89.7	283	2	S52928	XSUG1 protein - Af
22	26	89.7	286	2	D71502	UDP-3-O-[3-hydroxy
23	26	89.7	287	2	C81615	UDP-3-O-(3-hydroxy
24	26	89.7	291	2	A81662	UDP-3-O-(3-hydroxy
25	26	89.7	315	2	S74513	hypothetical prote
26	26	89.7	318	2	G70131	hypothetical prote
27	26	89.7	321	2	T52537	arginase (EC 3.5.3
28	26	89.7	323	1	S45455	arginase (EC 3.5.3
29	26	89.7	323	2	T38739	arginase - fission
30	26	89.7	324	2	G43354	pregnancy-specific
31	26	89.7	326	2	F43354	pregnancy-specific
32	26	89.7	326	2	JC4124	pregnancy-specific
33	26	89.7	332	2	JN0067	pregnancy-specific
34	26	89.7	333	2	A43354	pregnancy-specific
35	26	89.7	335	2	A33514	pregnancy-specific
36	26	89.7	335	2	H43354	pregnancy-specific
37	26	89.7	335	2	B33251	nonspecific cross-
38	26	89.7	335	2	C54312	pregnancy-specific
39	26	89.7	336	2	C27658	pregnancy-specific
40	26	89.7	348	2	T26447	hypothetical prote
41	26	89.7	352	2	I77374	pregnancy-specific
42	26	89.7	374	2	T43799	proteasome protein
43	26	89.7	389	2	JN0610	probable transcrip
44	26	89.7	395	2	D43354	pregnancy-specific
45	26	89.7	397	2	C43354	pregnancy-specific

ALIGNMENTS

RESULT 1
G90774
hypothetical protein ECs1167 [imported] - Escherichia coli (strain O157:H7, substrain
C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
C;Accession: G90774
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and g
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: G90774
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-95 <HAY>
A;Cross-references: GB:BA000007; PIDN:BAB34590.1; PID:g13360627; GSPDB:GN00154
A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
A;Gene: ECs1167

Query Match 100.0%; Score 29; DB 2; Length 95;
Best Local Similarity 100.0%; Pred. No. 7.7;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYTMH 5
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Db 30 SYTMH 34

RESULT 2
S17230
Ig heavy chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 06-Jun-1997
C;Accession: S17230
R;Clackson, T.; Hoogenboom, H.R.; Griffiths, A.D.; Winter, G.
Nature 352, 624-628, 1991
A;Title: Making antibody fragments using phage display libraries.
A;Reference number: S17230; MUID:91326098; PMID:1907718
A;Accession: S17230
A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-96 <CLA>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;8-91/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 29; DB 2; Length 96;
Best Local Similarity 100.0%; Pred. No. 7.8;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYTMH 5

GenCore version 5.1.4_p5_4578

OM protein - protein search, using sw model

Run on: April 16, 2003, 16:56:17 ; Search time 3.96491 Seconds
(without alignments)
168.037 Million cell updates/sec

Title: US-09-644-668A-27
Perfect score: 29
Sequence: 1 SYTMH 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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23: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	29	100.0	5	20	AAW90315	Human anti-idiotyp
2	29	100.0	5	22	AAB67490	Human heavy chain
3	29	100.0	78	23	ABP34671	Human ORF3644 prot
4	29	100.0	114	13	AAR21264	Murine VH group 1
5	29	100.0	114	13	AAR21283	Murine VH group 1
6	29	100.0	114	13	AAR21284	Murine VH group 1
7	29	100.0	118	22	AAB67508	Light chain variab
8	29	100.0	118	22	AAB67509	Light chain variab
9	29	100.0	118	22	AAB67513	Heavy chain variab
10	29	100.0	118	22	AAB67514	Heavy chain variab
11	29	100.0	120	17	AAW05825	Humanised M291 ant
12	29	100.0	124	20	AAW90285	Human anti-GPIIb/I
13	29	100.0	135	13	AAR24107	Humanised anti-Tac
14	29	100.0	139	19	AAW36165	Humanised heavy ch
15	29	100.0	139	19	AAW36167	Heavy chain variab
16	29	100.0	214	20	AAY44176	MAb Fab13B5 heavy
17	29	100.0	279	17	AAW05826	Humanised M291 ant
18	29	100.0	296	20	AAY27073	L. bimastus plasmi
19	26	89.7	34	22	ABG18515	Novel human diagno
20	26	89.7	34	22	AAO08358	Human polypeptide
21	26	89.7	37	22	AAM86640	Human immune/haema
22	26	89.7	56	21	AAG59811	Arabidopsis thalia
23	26	89.7	77	23	ABP38145	Staphylococcus epi
24	26	89.7	83	22	AAM88306	Human immune/haema
25	26	89.7	112	22	AAU32900	Novel human secret
26	26	89.7	122	12	AAR13161	Pregnancy-specific
27	26	89.7	125	21	AAG00868	Human secreted pro
28	26	89.7	144	11	AAR06431	N-terminal of SP1-
29	26	89.7	166	20	AAY35272	Chlamydia pneumoni
30	26	89.7	167	22	ABB50914	Human secreted pro
31	26	89.7	183	22	ABG21057	Novel human diagno
32	26	89.7	208	20	AAY37686	C. trachomatis lip
33	26	89.7	228	16	AAR74631	Tomato TGETR2 ethy
34	26	89.7	228	19	AAW73127	Tomato ethylene re
35	26	89.7	238	21	AAY79247	Caenorhabditis ele
36	26	89.7	248	11	AAR06433	SP1-like protein e
37	26	89.7	281	21	AAB00203	Putative polyunsat
38	26	89.7	281	21	AAB00212	Potential polyunsa
39	26	89.7	315	22	AAB68291	Amino acid sequenc
40	26	89.7	324	22	AAM93561	Human polypeptide,
41	26	89.7	326	22	AAM93510	Human polypeptide,
42	26	89.7	326	22	AAM93575	Human polypeptide,
43	26	89.7	335	21	AAY57912	Human transmembran
44	26	89.7	355	22	ABG18511	Novel human diagno
45	26	89.7	399	22	ABB58875	Drosophila melanog

ALIGNMENTS

RESULT 1
AAW90315
ID AAW90315 standard; Protein; 5 AA.
XX
AC AAW90315;
XX
DT 07-SEP-1999 (first entry)
XX
DE Human anti-idiotypic antibody heavy chain protein CDR1 region 2.
XX
KW Antibody; GPIIb/IIIa; human; auto-antibody; anti-idiotypic; diagnosis;
KW blood platelet membrane protein; predisposition; prevention; treatment;
KW autoimmune thrombocytopaenic purpura; AITP; fibrinogen binding; thrombi;
KW thrombocyte; cardiac infarction; pulmonary embolism; heavy chain; CDR1.
XX
OS Homo sapiens.
XX
PN WO9855619-A1.
XX
PD 10-DEC-1998.
XX
PF 05-JUN-1998; 98WO-EP03397.
XX
PR 08-MAY-1998; 98DE-1020663.
PR 06-JUN-1997; 97DE-1023904.
PR 12-DEC-1997; 97DE-1055227.
XX
PA (ASAT-) ASAT AG APPLIED SCI & TECHNOLOGY.
XX
PI Berchtold P, Escher RFA;
XX
DR WPI; 1999-105496/09.
XX

```
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray & Borun
;       STREET:  6300 Sears Tower, 233 South Wacker Drive
;       CITY:  Chicago
;       STATE:  Illinois
;       COUNTRY:  USA
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25 (EPO)
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/09/098,244
;       FILING DATE:  17-JUN-1998
;       CLASSIFICATION:  435
;       CLASSIFICATION:  16/00, A61K 39/395
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/889,291
;       FILING DATE:  08-JUL-1997
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  PCT/GB97/01835
;       FILING DATE:  08-JUL-1997
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  GB 9614292.2
;       FILING DATE:  08-JUL-1996
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  GB 9624880.2
;       FILING DATE:  29-NOV-1996
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  GB 9712818.5
;       FILING DATE:  18-JUN-1997
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  David W. Clough
;       REGISTRATION NUMBER:  36,107
;       REFERENCE/DOCKET NUMBER:  28111/34800
;   INFORMATION FOR SEQ ID NO:  8:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  32 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
US-09-098-244-8

  Query Match             89.7%;  Score 26;  DB 4;  Length 32;
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Qy       1 SYTMH 5
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Db       9 SYTLH 13


RESULT 8
US-09-375-314-8
; Sequence 8, Application US/09375314
; Patent No. 6342588
;  GENERAL INFORMATION:
;     APPLICANT:  Osbourn, Jane K
;     APPLICANT:  Derbyshire, Elaine J
;     APPLICANT:  McCafferty, John G
;     APPLICANT:  Vaughan, Tristan J
;     APPLICANT:  Johnson, Kevin S
;     TITLE OF INVENTION:  Labelling and selection of molecules
;     NUMBER OF SEQUENCES:  36
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray & Borun
;       STREET:  6300 Sears Tower, 233 South Wacker Drive
;       CITY:  Chicago
;       STATE:  Illinois
;       COUNTRY:  USA
;       ZIP:  60606-6402
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25 (EPO)
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/09/375,314
;       FILING DATE:
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;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/889,291
;       FILING DATE:  08-JUL-1997
;       APPLICATION NUMBER:  PCT/GB97/01835
;       FILING DATE:  08-JUL-1997
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  GB 9614292.2
;       FILING DATE:  08-JUL-1996
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  GB 9624880.2
;       FILING DATE:  29-NOV-1996
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  GB 9712818.5
;       FILING DATE:  18-JUN-1997
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  David W. Clough
;       REGISTRATION NUMBER:  36,107
;       REFERENCE/DOCKET NUMBER:  28111/34063
;   INFORMATION FOR SEQ ID NO:  8:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  32 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
US-09-375-314-8

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Qy       1 SYTMH 5
           |||:|
Db       9 SYTLH 13


RESULT 9
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; Patent No. 6380370
; GENERAL INFORMATION:
;  APPLICANT: Lynn Doucette-Stamm et al
;  TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
;  TITLE OF INVENTION:  EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE: GTC-007
;  CURRENT APPLICATION NUMBER: US/09/134,001C
;  CURRENT FILING DATE:  1998-08-13
;  PRIOR APPLICATION NUMBER: US 60/064,964
;  PRIOR FILING DATE: 1997-11-08
;  PRIOR APPLICATION NUMBER: US 60/055,779
;  PRIOR FILING DATE: 1997-08-14
;  NUMBER OF SEQ ID NOS: 5674
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;   LENGTH: 77
;   TYPE: PRT
;   ORGANISM: Staphylococcus epidermidis
US-09-134-001C-2990

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Qy       1 SYTMH 5
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Db      62 SYTLH 66


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;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  139 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-656-586-8

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  Best Local Similarity   100.0%;  Pred. No. 20;
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Qy       1 SYTMH 5
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Db      50 SYTMH 54


RESULT 5
US-08-397-411-13
; Sequence 13, Application US/08397411
; Patent No. 6129914
; GENERAL INFORMATION:
;    APPLICANT:  Weiner, George
;    APPLICANT:  Gingrich, Roger
;    APPLICANT:  Link, Brian
;    APPLICANT:  Tso, J. Yun
;    TITLE OF INVENTION:  Bispecific Antibody Effective to Treat
;    TITLE OF INVENTION:  B-Cell Lymphoma and Cell Line
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew
;      STREET:  One Market Plaza, Steuart Tower, Suite 2000
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94105
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/397,411
;      FILING DATE:  01-MAR-1995
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/859,583
;      FILING DATE:  27-MAR-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William M.
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  011823-004901
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-326-2400
;      TELEFAX:  415-326-2422
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  279 amino acids
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US-08-397-411-13

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Qy       1 SYTMH 5
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Db      31 SYTMH 35


RESULT 6
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; Sequence 8, Application US/08889291
; Patent No. 5994519
; GENERAL INFORMATION:
;    APPLICANT:  Osbourn, Jane K
;    APPLICANT:  Derbyshire, Elaine J
;    APPLICANT:  McCafferty, John G
;    APPLICANT:  Vaughan, Tristan J
;    APPLICANT:  Johnson, Kevin S
;    TITLE OF INVENTION:  Labelling and selection of molecules
;    NUMBER OF SEQUENCES:  36
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray & Borun
;      STREET:  6300 Sears Tower, 233 South Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25 (EPO)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/889,291
;      FILING DATE:  08-JUL-1997
;      CLASSIFICATION:  435
;      CLASSIFICATION:  16/00, A61K 39/395
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/GB97/01835
;      FILING DATE:  08-JUL-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9614292.2
;      FILING DATE:  08-JUL-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9624880.2
;      FILING DATE:  29-NOV-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9712818.5
;      FILING DATE:  18-JUN-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  David W. Clough
;      REGISTRATION NUMBER:  36,107
;      REFERENCE/DOCKET NUMBER:  28111/34063
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  32 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
US-08-889-291-8

  Query Match             89.7%;  Score 26;  DB 2;  Length 32;
  Best Local Similarity   80.0%;  Pred. No. 20;
  Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 SYTMH 5
           |||:|
Db       9 SYTLH 13


RESULT 7
US-09-098-244-8
; Sequence 8, Application US/09098244
; Patent No. 6180336
; GENERAL INFORMATION:
;    APPLICANT:  Osbourn, Jane K
;    APPLICANT:  Derbyshire, Elaine J
;    APPLICANT:  McCafferty, John G
;    APPLICANT:  Vaughan, Tristan J
;    APPLICANT:  Johnson, Kevin S
;    TITLE OF INVENTION:  Labelling and selection of molecules
;    NUMBER OF SEQUENCES:  36
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Qy       1 SYTMH 5
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Db      31 SYTMH 35


RESULT 2
US-08-397-411-11
; Sequence 11, Application US/08397411
; Patent No. 6129914
;  GENERAL INFORMATION:
;    APPLICANT:  Weiner, George
;    APPLICANT:  Gingrich, Roger
;    APPLICANT:  Link, Brian
;    APPLICANT:  Tso, J. Yun
;    TITLE OF INVENTION:  Bispecific Antibody Effective to Treat
;    TITLE OF INVENTION:  B-Cell Lymphoma and Cell Line
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew
;      STREET:  One Market Plaza, Steuart Tower, Suite 2000
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94105
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/397,411
;      FILING DATE:  01-MAR-1995
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/859,583
;      FILING DATE:  27-MAR-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William M.
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  011823-004901
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-326-2400
;      TELEFAX:  415-326-2422
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  120 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-397-411-11

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Qy       1 SYTMH 5
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Db      31 SYTMH 35


RESULT 3
US-08-656-586-4
; Sequence 4, Application US/08656586
; Patent No. 5834597
;  GENERAL INFORMATION:
;    APPLICANT:  Tso, J. Yun
;    APPLICANT:  Cole, Michael S.
;    APPLICANT:  Anasetti, Claudio
;    TITLE OF INVENTION:  Mutated No. 5834597activating IgG2 Domains and
;    TITLE OF INVENTION:  Anti-CD3 Antibodies Incorporating the Same
;    NUMBER OF SEQUENCES:  13
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/656,586
;      FILING DATE:  31-MAY-1996
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Liebeschuetz, Joseph O.
;      REGISTRATION NUMBER:  37,505
;      REFERENCE/DOCKET NUMBER:  11823-007210US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  139 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-656-586-4

  Query Match             100.0%;  Score 29;  DB 2;  Length 139;
  Best Local Similarity   100.0%;  Pred. No. 20;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 SYTMH 5
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Db      50 SYTMH 54


RESULT 4
US-08-656-586-8
; Sequence 8, Application US/08656586
; Patent No. 5834597
;  GENERAL INFORMATION:
;    APPLICANT:  Tso, J. Yun
;    APPLICANT:  Cole, Michael S.
;    APPLICANT:  Anasetti, Claudio
;    TITLE OF INVENTION:  Mutated No. 5834597activating IgG2 Domains and
;    TITLE OF INVENTION:  Anti-CD3 Antibodies Incorporating the Same
;    NUMBER OF SEQUENCES:  13
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/656,586
;      FILING DATE:  31-MAY-1996
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Liebeschuetz, Joseph O.
;      REGISTRATION NUMBER:  37,505
;      REFERENCE/DOCKET NUMBER:  11823-007210US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
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GenCore version 5.1.4_p5_4578

OM protein - protein search, using sw model

Run on: April 16, 2003, 17:15:40 ; Search time 1.2807 Seconds
(without alignments)
114.870 Million cell updates/sec

Title: US-09-644-668A-27
Perfect score: 29
Sequence: 1 SYTMH 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	29	100.0	120	3	US-08-397-411-10	Sequence 10, Appl
2	29	100.0	120	3	US-08-397-411-11	Sequence 11, Appl
3	29	100.0	139	2	US-08-656-586-4	Sequence 4, Appli
4	29	100.0	139	2	US-08-656-586-8	Sequence 8, Appli
5	29	100.0	279	3	US-08-397-411-13	Sequence 13, Appl
6	26	89.7	32	2	US-08-889-291-8	Sequence 8, Appli
7	26	89.7	32	4	US-09-098-244-8	Sequence 8, Appli
8	26	89.7	32	4	US-09-375-314-8	Sequence 8, Appli
9	26	89.7	77	4	US-09-134-001C-2990	Sequence 2990, Ap
10	26	89.7	122	6	5169835-12	Patent No. 5169835
11	26	89.7	143	6	5169835-18	Patent No. 5169835
12	26	89.7	144	6	5169835-8	Patent No. 5169835
13	26	89.7	228	2	US-08-484-101B-40	Sequence 40, Appl
14	26	89.7	228	4	US-08-714-524D-40	Sequence 40, Appl
15	26	89.7	238	4	US-09-145-828A-13	Sequence 13, Appl
16	26	89.7	248	6	5169835-15	Patent No. 5169835
17	26	89.7	315	4	US-09-434-774-16	Sequence 16, Appl
18	26	89.7	406	2	US-08-222-719-1	Sequence 1, Appli
19	26	89.7	406	2	US-08-470-925-1	Sequence 1, Appli
20	26	89.7	406	2	US-08-471-613-1	Sequence 1, Appli
21	26	89.7	406	5	PCT-US93-10443-1	Sequence 1, Appli
22	26	89.7	419	6	5169835-2	Patent No. 5169835
23	26	89.7	424	6	5169835-6	Patent No. 5169835
24	26	89.7	490	4	US-09-292-225-41	Sequence 41, Appl
25	26	89.7	505	1	US-09-041-075A-8	Sequence 8, Appli
26	26	89.7	509	4	US-09-292-225-35	Sequence 35, Appl
27	26	89.7	509	4	US-09-292-225-38	Sequence 38, Appl
28	26	89.7	536	4	US-09-292-225-21	Sequence 21, Appl
29	26	89.7	555	4	US-09-292-225-15	Sequence 15, Appl
30	26	89.7	555	4	US-09-292-225-18	Sequence 18, Appl
31	25	86.2	23	4	US-09-292-225-9	Sequence 9, Appli
32	25	86.2	54	4	US-09-516-352A-2	Sequence 2, Appli
33	25	86.2	67	1	US-08-162-102C-37	Sequence 37, Appl
34	25	86.2	85	2	US-08-480-229C-3	Sequence 3, Appli
35	25	86.2	85	2	US-08-659-235C-3	Sequence 3, Appli
36	25	86.2	111	1	US-08-111-939-23	Sequence 23, Appl
37	25	86.2	117	4	US-08-525-539A-76	Sequence 76, Appl
38	25	86.2	117	4	US-08-525-539A-78	Sequence 78, Appl
39	25	86.2	118	1	US-08-491-845-6	Sequence 6, Appli
40	25	86.2	118	1	US-08-491-845-14	Sequence 14, Appl
41	25	86.2	118	2	US-08-116-247-10	Sequence 10, Appl
42	25	86.2	118	3	US-08-545-809A-125	Sequence 125, App
43	25	86.2	119	2	US-08-303-569B-11	Sequence 11, Appl
44	25	86.2	119	2	US-08-303-569B-12	Sequence 12, Appl
45	25	86.2	119	2	US-08-303-569B-13	Sequence 13, Appl

ALIGNMENTS

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RESULT 1
US-08-397-411-10
; Sequence 10, Application US/08397411
; Patent No. 6129914
;  GENERAL INFORMATION:
;    APPLICANT:  Weiner, George
;    APPLICANT:  Gingrich, Roger
;    APPLICANT:  Link, Brian
;    APPLICANT:  Tso, J. Yun
;    TITLE OF INVENTION:  Bispecific Antibody Effective to Treat
;    TITLE OF INVENTION:  B-Cell Lymphoma and Cell Line
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew
;      STREET:  One Market Plaza, Steuart Tower, Suite 2000
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94105
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/397,411
;      FILING DATE:  01-MAR-1995
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/859,583
;      FILING DATE:  27-MAR-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William M.
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  011823-004901
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-326-2400
;      TELEFAX:  415-326-2422
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  120 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-397-411-10

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  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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RESULT 2
US-08-488-113B-150
; Sequence 150, Application US/08488113B
; Patent No. 5744580
;  GENERAL INFORMATION:
;    APPLICANT:  Better, Marc D.
;    APPLICANT:  Carroll, Stephen F.
;    APPLICANT:  Studnika, Gary M.
;    TITLE OF INVENTION:  Immunotoxins Comprising Ribosome-Inactivating
;    TITLE OF INVENTION:  Proteins
;    NUMBER OF SEQUENCES:  169
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  McAndrews, Held & Malloy, Ltd.
;      STREET:  500 West Madison Street, 34th floor
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60661
;     COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/488,113B
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/425,336
;      FILING DATE:  18-APR-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/064,691
;      FILING DATE:  12-MAY-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/988,430
;      FILING DATE:  09-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/901,707
;      FILING DATE:  19-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/787,567
;      FILING DATE:  04-NOV-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McNicholas, Janet M.
;      REGISTRATION NUMBER:  32,918
;      REFERENCE/DOCKET NUMBER:  11022US07/200-70.P3.C2A
;     ELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/707-8889
;      TELEFAX:  312/707-9155
;      TELEX:  650 388-1248
;  INFORMATION FOR SEQ ID NO:  150:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  108 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-488-113B-150

  Query Match             89.1%;  Score 49;  DB 1;  Length 108;
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  Matches   11;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

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Db      24 RASQSVSSSYLA 35


RESULT 3
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; Sequence 150, Application US/08477484B
; Patent No. 5756699
;  GENERAL INFORMATION:
;    APPLICANT:  Better, Marc D.
;    APPLICANT:  Carroll, Stephen F.
;    APPLICANT:  Studnika, Gary M.
;    TITLE OF INVENTION:  Immunotoxins Comprising Ribosome-Inactivating
;    TITLE OF INVENTION:  Proteins
;    NUMBER OF SEQUENCES:  169
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  McAndrews, Held & Malloy, Ltd.
;      STREET:  500 West Madison Street, 34th floor
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60661
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/477,484B
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/425,336
;      FILING DATE:  18-APR-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/064,691
;      FILING DATE:  12-MAY-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/988,430
;      FILING DATE:  09-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/901,707
;      FILING DATE:  19-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/787,567
;      FILING DATE:  04-NOV-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McNicholas, Janet M.
;      REGISTRATION NUMBER:  32,918
;      REFERENCE/DOCKET NUMBER:  11022US07/200-70.P3.C2A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/707-8889
;      TELEFAX:  312/707-9155
;      TELEX:  650 388-1248
;  INFORMATION FOR SEQ ID NO:  150:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  108 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-477-484B-150

  Query Match             89.1%;  Score 49;  DB 1;  Length 108;
  Best Local Similarity   91.7%;  Pred. No. 0.031;
  Matches   11;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 RASQSVGSSYLA 12
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Db      24 RASQSVSSSYLA 35


RESULT 4
US-08-646-360-150
; Sequence 150, Application US/08646360
; Patent No. 5837491
;  GENERAL INFORMATION:
;    APPLICANT:  Better, Marc D.
;    APPLICANT:  Carroll, Stephen F.
;    APPLICANT:  Studnika, Gary M.
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GenCore version 5.1.4_p5_4578

OM protein - protein search, using sw model

Run on: April 16, 2003, 17:15:40 ; Search time 3.07368 Seconds
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114.870 Million cell updates/sec

Title: US-09-644-668A-24
Perfect score: 55
Sequence: 1 RASQSVGSSYLA 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	49	89.1	108	1	US-08-477-484B-150	Sequence 150, App
4	49	89.1	108	2	US-08-646-360-150	Sequence 150, App
5	49	89.1	108	2	US-08-232-081B-42	Sequence 42, Appl
6	49	89.1	108	4	US-08-839-765-150	Sequence 150, App
7	49	89.1	108	4	US-09-136-389-150	Sequence 150, App
8	49	89.1	108	4	US-09-610-838-150	Sequence 150, App
9	49	89.1	109	4	US-09-025-769B-16	Sequence 16, Appl
10	49	89.1	110	4	US-09-025-769B-30	Sequence 30, Appl
11	49	89.1	110	4	US-09-025-769B-47	Sequence 47, Appl
12	49	89.1	116	1	US-08-053-131-183	Sequence 183, App
13	49	89.1	116	2	US-08-096-762-183	Sequence 183, App
14	49	89.1	116	4	US-09-042-353-46	Sequence 46, Appl
15	49	89.1	116	4	US-08-758-417A-311	Sequence 311, App
16	49	89.1	150	4	US-08-862-124-5	Sequence 5, Appli
17	49	89.1	287	4	US-08-862-124-17	Sequence 17, Appl
18	49	89.1	304	4	US-08-862-124-14	Sequence 14, Appl
19	48	87.3	108	4	US-09-240-274-178	Sequence 178, App
20	46	83.6	109	1	US-08-276-852-147	Sequence 147, App
21	46	83.6	109	1	US-08-899-575-147	Sequence 147, App
22	46	83.6	109	1	US-08-899-575-147	Sequence 147, App
23	46	83.6	109	5	PCT-US95-08743-147	Sequence 147, App
24	45	81.8	112	1	US-08-276-852-151	Sequence 151, App
25	45	81.8	112	1	US-08-899-575-151	Sequence 151, App
26	45	81.8	112	1	US-08-899-575-151	Sequence 151, App
27	45	81.8	112	5	PCT-US95-08743-151	Sequence 151, App
28	44	80.0	129	2	US-08-480-774A-4	Sequence 4, Appl
29	43	78.2	107	1	US-08-276-852-87	Sequence 87, Appl
30	43	78.2	107	1	US-08-899-575-87	Sequence 87, Appl
31	43	78.2	107	1	US-08-899-575-87	Sequence 87, Appl
32	43	78.2	107	5	PCT-US95-08743-87	Sequence 87, Appl
33	42	76.4	57	1	US-08-162-102C-38	Sequence 38, Appl
34	42	76.4	105	1	US-08-276-852-93	Sequence 93, Appl
35	42	76.4	105	1	US-08-899-575-93	Sequence 93, Appl
36	42	76.4	105	1	US-08-899-575-93	Sequence 93, Appl
37	42	76.4	105	5	PCT-US95-08743-93	Sequence 93, Appl
38	42	76.4	108	1	US-08-276-852-86	Sequence 86, Appl
39	42	76.4	108	1	US-08-899-575-86	Sequence 86, Appl
40	42	76.4	108	1	US-08-899-575-86	Sequence 86, Appl
41	42	76.4	108	5	PCT-US95-08743-86	Sequence 86, Appl
42	42	76.4	109	1	US-08-162-102C-23	Sequence 23, Appl
43	42	76.4	109	5	PCT-US93-08786-23	Sequence 23, Appl
44	42	76.4	111	1	US-08-276-852-149	Sequence 149, App
45	42	76.4	111	1	US-08-899-575-149	Sequence 149, App

ALIGNMENTS

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RESULT 1
US-08-652-558-49
; Sequence 49, Application US/08652558
; Patent No. 5861155
;  GENERAL INFORMATION:
;    APPLICANT:  LIN, AUGUSTINE YEE-THARN
;    TITLE OF INVENTION:  HUMANIZED ANTIBODIES AND USES
;    TITLE OF INVENTION:  THEREOF
;    NUMBER OF SEQUENCES:  52
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BANNER & WITCOFF
;      STREET:  75 STATE STREET, 23RD FLOOR
;      CITY:  BOSTON
;      STATE:  MASSACHUSETTS
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch diskette, 1.4 Mb storage
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WordPerfect 6.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/652,558
;      FILING DATE:  JUNE 6, 1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/IB94/00387
;      FILING DATE:  NOVEMBER 21, 1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  YANKWICH, LEON R.
;      REGISTRATION NUMBER:  30,237
;      REFERENCE/DOCKET NUMBER:  95,497-L
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-345-9100
;      TELEFAX:  617-345-9111
;  INFORMATION FOR SEQ ID NO:  49:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  107 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-652-558-49

  Query Match             89.1%;  Score 49;  DB 2;  Length 107;
  Best Local Similarity   91.7%;  Pred. No. 0.03;
  Matches   11;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 RASQSVGSSYLA 12
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Db      24 RASQSVSSSYLA 35
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;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 38
;    LENGTH: 12
;    TYPE: PRT
;    ORGANISM: Homo sapiens
US-09-828-708-38

  Query Match             89.1%;  Score 49;  DB 10;  Length 12;
  Best Local Similarity   91.7%;  Pred. No. 0.013;
  Matches   11;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 RASQSVGSSYLA 12
           |||||| |||||
Db       1 RASQSVSSSYLA 12


RESULT 3
US-09-828-708-40
; Sequence 40, Application US/09828708
;      nt No. US20020146753A1
; G    RAL INFORMATION:
;  APPLICANT: Ditzel, H.
;  APPLICANT:  Burton, D.
;  APPLICANT:  Schaller, M.
;  TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their partici
;  TITLE OF INVENTION:  autoimmune disease
;  FILE REFERENCE: 1361.005US1
;  CURRENT APPLICATION NUMBER: US/09/828,708
;  CURRENT FILING DATE:  2001-09-24
;  NUMBER OF SEQ ID NOS: 123
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 40
;    LENGTH: 12
;    TYPE: PRT
;    ORGANISM: Homo sapiens
US-09-828-708-40

  Query Match             89.1%;  Score 49;  DB 10;  Length 12;
  Best Local Similarity   91.7%;  Pred. No. 0.013;
  Matches   11;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 RASQSVGSSYLA 12
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Db       1 RASQSVSSSYLA 12


RESULT 4
US     828-708-41
;      ience 41, Application US/09828708
; Patent No. US20020146753A1
; GENERAL INFORMATION:
;  APPLICANT: Ditzel, H.
;  APPLICANT:  Burton, D.
;  APPLICANT:  Schaller, M.
;  TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their partici
;  TITLE OF INVENTION:  autoimmune disease
;  FILE REFERENCE: 1361.005US1
;  CURRENT APPLICATION NUMBER: US/09/828,708
;  CURRENT FILING DATE:  2001-09-24
;  NUMBER OF SEQ ID NOS: 123
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 41
;    LENGTH: 12
;    TYPE: PRT
;    ORGANISM: Homo sapiens
US-09-828-708-41

  Query Match             89.1%;  Score 49;  DB 10;  Length 12;
  Best Local Similarity   91.7%;  Pred. No. 0.013;
  Matches   11;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 RASQSVGSSYLA 12
           |||||| |||||
Db       1 RASQSVSSSYLA 12


RESULT 5
US-09-828-708-42
; Sequence 42, Application US/09828708
; Patent No. US20020146753A1
; GENERAL INFORMATION:
;  APPLICANT: Ditzel, H.
;  APPLICANT:  Burton, D.
;  APPLICANT:  Schaller, M.
;  TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their partici
;  TITLE OF INVENTION:  autoimmune disease
;  FILE REFERENCE: 1361.005US1
;  CURRENT APPLICATION NUMBER: US/09/828,708
;  CURRENT FILING DATE:  2001-09-24
;  NUMBER OF SEQ ID NOS: 123
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 42
;    LENGTH: 12
;    TYPE: PRT
;    ORGANISM: Homo sapiens
US-09-828-708-42

  Query Match             89.1%;  Score 49;  DB 10;  Length 12;
  Best Local Similarity   91.7%;  Pred. No. 0.013;
  Matches   11;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 RASQSVGSSYLA 12
           |||||| |||||
Db       1 RASQSVSSSYLA 12


RESULT 6
US-10-125-687-23
; Sequence 23, Application US/10125687
; Publication No. US20030054407A1
; GENERAL INFORMATION:
;  APPLICANT: Luo, Peter
;  TITLE OF INVENTION: STRUCTURE-BASED CONSTRUCTION OF HUMAN ANTIBODY LIBRARY
;  FILE REFERENCE: 26050-705
;  CURRENT APPLICATION NUMBER: US/10/125,687
;  CURRENT FILING DATE:  2002-04-17
;  NUMBER OF SEQ ID NOS: 28
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
;    LENGTH: 74
;    TYPE: PRT
;    ORGANISM: Homo sapiens
US-10-125-687-23

  Query Match             89.1%;  Score 49;  DB 9;  Length 74;
  Best Local Similarity   91.7%;  Pred. No. 0.076;
  Matches   11;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 RASQSVGSSYLA 12
           |||||| |||||
Db      17 RASQSVSSSYLA 28


RESULT 7
US-10-025-687-23
; Sequence 23, Application US/10025687
; Patent No. US20020142255A1
; GENERAL INFORMATION:
;  APPLICANT: Luo, Peter
;  TITLE OF INVENTION: STRUCTURE-BASED CONSTRUCTION OF HUMAN ANTIBODY LIBRARY
;  FILE REFERENCE: 26050-705
;  CURRENT APPLICATION NUMBER: US/10/025,687
;  CURRENT FILING DATE:  2002-04-17
;  NUMBER OF SEQ ID NOS: 28
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
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GenCore version 5.1.4_p5_4578

OM protein - protein search, using sw model

Run on: April 16, 2003, 17:21:54 ; Search time 3.53684 Seconds
(without alignments)
256.547 Million cell updates/sec

Title: US-09-644-668A-24
Perfect score: 55
Sequence: 1 RASQSVGSSYLA 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 288829 seqs, 75613885 residues

Total number of hits satisfying chosen parameters: 288829

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
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7: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
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11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
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13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	49	89.1	12	9	US-10-001-934-62	Sequence 62, Appl
2	49	89.1	12	10	US-09-828-708-38	Sequence 38, Appl
3	49	89.1	12	10	US-09-828-708-40	Sequence 40, Appl
4	49	89.1	12	10	US-09-828-708-41	Sequence 41, Appl
5	49	89.1	12	10	US-09-828-708-42	Sequence 42, Appl
6	49	89.1	74	9	US-10-125-687-23	Sequence 23, Appl
7	49	89.1	74	12	US-10-025-687-23	Sequence 23, Appl
8	49	89.1	96	9	US-10-194-975-82	Sequence 82, Appl
9	49	89.1	104	10	US-09-828-708-6	Sequence 6, Appli
10	49	89.1	105	10	US-09-828-708-3	Sequence 3, Appli
11	49	89.1	105	10	US-09-828-708-5	Sequence 5, Appli
12	49	89.1	105	10	US-09-828-708-7	Sequence 7, Appli
13	49	89.1	108	9	US-09-300-425B-21	Sequence 21, Appl
14	49	89.1	109	9	US-10-125-687-10	Sequence 10, Appl
15	49	89.1	109	12	US-10-025-687-10	Sequence 10, Appl
16	49	89.1	110	9	US-10-001-934-40	Sequence 40, Appl
17	49	89.1	150	9	US-09-782-397-5	Sequence 5, Appli
18	49	89.1	246	9	US-09-880-748-1264	Sequence 1264, Ap
19	49	89.1	251	9	US-09-880-748-1219	Sequence 1219, Ap
20	49	89.1	252	9	US-09-880-748-1534	Sequence 1534, Ap
21	49	89.1	287	9	US-09-782-397-17	Sequence 17, Appl
22	49	89.1	304	9	US-09-782-397-14	Sequence 14, Appl
23	48	87.3	108	9	US-09-848-798-178	Sequence 178, App
24	48	87.3	245	9	US-09-880-748-1896	Sequence 1896, Ap
25	46	83.6	96	9	US-10-194-975-88	Sequence 88, Appl
26	46	83.6	107	8	US-08-844-215-8	Sequence 8, Appli
27	44	80.0	12	9	US-09-977-797A-24	Sequence 24, Appl
28	44	80.0	96	9	US-10-194-975-83	Sequence 83, Appl
29	44	80.0	253	9	US-09-880-748-1499	Sequence 1499, Ap
30	43	78.2	236	10	US-09-859-053-34	Sequence 34, Appl
31	43	78.2	254	9	US-09-880-748-905	Sequence 905, App
32	42	76.4	106	8	US-08-844-215-14	Sequence 14, Appl
33	40	72.7	109	9	US-09-144-886-91	Sequence 91, Appl
34	40	72.7	109	9	US-10-141-908-8	Sequence 8, Appli
35	40	72.7	146	9	US-09-925-299-776	Sequence 776, App
36	40	72.7	146	10	US-09-925-299-776	Sequence 776, App
37	39	70.9	11	9	US-09-968-561A-298	Sequence 298, App
38	39	70.9	11	10	US-09-192-854-170	Sequence 170, App
39	39	70.9	88	10	US-09-905-243-30	Sequence 30, Appl
40	39	70.9	95	9	US-10-194-975-91	Sequence 91, Appl
41	39	70.9	95	9	US-10-194-975-92	Sequence 92, Appl
42	39	70.9	107	8	US-08-844-215-10	Sequence 10, Appl
43	39	70.9	236	10	US-09-859-053-38	Sequence 38, Appl
44	39	70.9	249	9	US-09-880-748-1035	Sequence 1035, Ap
45	38.5	70.0	95	9	US-10-194-975-86	Sequence 86, Appl

ALIGNMENTS

RESULT 1
US-10-001-934-62
; Sequence 62, Application US/10001934
; Publication No. US20030032782A1
; GENERAL INFORMATION:
; APPLICANT: NAGY, ZOLTAN
; TITLE OF INVENTION: HUMAN PEPTIDES/PROTEINS CAUSING OR LEADING TO THE
; TITLE OF INVENTION: KILLING OF CELLS INCLUDING LYMPHOID TUMOR CELLS
; FILE REFERENCE: GPCG-P01-003
; CURRENT APPLICATION NUMBER: US/10/001,934
; CURRENT FILING DATE: 2001-11-15
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 62
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-001-934-62

Query Match 89.1%; Score 49; DB 9; Length 12;
Best Local Similarity 91.7%; Pred. No. 0.013;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQSVGSSYLA 12
||||||.|||||
Db 1 RASQSVSSSYLA 12

RESULT 2
US-09-828-708-38
; Sequence 38, Application US/09828708
; Patent No. US20020146753A1
; GENERAL INFORMATION:
; APPLICANT: Ditzel, H.
; APPLICANT: Burton, D.
; APPLICANT: Schaller, M.
; TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their parti
; TITLE OF INVENTION: autoimmune disease
; FILE REFERENCE: 1361.005US1
; CURRENT APPLICATION NUMBER: US/09/828,708
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 123

PT Novel human sequence antibody that binds to human cytotoxic T
PT lymphocyte associated antigen-4, useful for inducing, augmenting or
PT prolonging immune response to antigen or for suppressing immune
PT response in patient -
XX
PS Claim 30; Page 99; 127pp; English.
XX
CC AAB67490-99 and AAB67501-06 represents complementarity determining
CC regions (CDRs) of human antibodies. The antibodies specifically bind to
CC human cytotoxic T lymphocyte associated antigen-4 (CTLA-4). Such
CC antibodies are used in methods for inducing, augmenting or prolonging
CC an immune response to an antigen in a patient, where the antibodies
CC block binding of human CTLA-4 to human B7 ligands. The antibodies are
CC also useful for treating autoimmune disease in a subject caused or
CC exacerbated by increased activity of T cells and for treating prostate
CC cancer, melanoma or epithelial cancer. A polyvalent or polyclonal
CC antibody preparation comprising two antibodies of the invention are
CC useful for suppressing a immune response in a patient. They are used for
CC treating cancer, infectious diseases and promoting beneficial autoimmune
CC reactions for the treatment of diseases with inflammatory or allergic
CC components. The polyvalent or polyclonal preparations are useful for
CC treating autoimmune diseases such as rheumatoid arthritis, myasthenia
CC gravis and lupus erythematosus, multiple sclerosis, insulin-dependent
CC diabetes mellitus, transplant rejection, and inflammation, graft versus
CC host disease.
XX
SQ Sequence 12 AA;

Query Match 100.0%; Score 55; DB 22; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQSVGSSYLA 12
||||||||||||
Db 1 RASQSVGSSYLA 12

RESULT 2
AAR15375
ID AAR15375 standard; Protein; 12 AA.
XX
AC AAR15375;
XX
DT 05-MAR-1992 (first entry)
XX
DE IgM-RF Glo.
XX
KW heumatoid factor; RF; antigen; CDR; IgM.
XX
OS Synthetic.
XX
PN US5068177-A.
XX
PD 26-NOV-1991.
XX
PF 05-AUG-1985; 85US-0762698.
XX
PR 05-AUG-1985; 85US-0762698.
PR 28-DEC-1983; 83US-0566172.
XX
PA (SCRI-) SCRIPPS CLINIC RES.
XX
PI Carson DA, Fong S, Chen PP;
XX
DR WPI; 1991-368612/50.
XX
PT Synthetic polypeptide(s) for inducing anti-idiotype antibodies -
PT useful for treating auto immune-, endocrine- and
PT rheumatic-diseases and myasthenia gravis
XX
PS Claim 10; Page 42; 44pp; English.
XX
CC Three rabbits were inoculated with two s.c. injections of PGL1
CC (synthetic peptide) conjugated to KLH as an immunogen, and their
CC sera were analysed for anti-peptide antibody activity by ELISA.
CC All three immunised rabbits produced anti-PGL1 antibody. Antisera
CC drawn from a rabbit on two different days reacted significantly with
CC the corresp. intact IgM-RF Glo.
CC See also AAR15365-74 and AAR15375.
XX
SQ Sequence 12 AA;

Query Match 89.1%; Score 49; DB 12; Length 12;
Best Local Similarity 91.7%; Pred. No. 0.003;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQSVGSSYLA 12
|||||| |||||
Db 1 RASQSVSSSYLA 12

RESULT 3
AAU83718
ID AAU83718 standard; Peptide; 12 AA.
XX
AC AAU83718;
XX
DT 08-MAY-2002 (first entry)
XX
DE MS-GPC-6 light chain variable region CD1 sequence.
XX
KW Human; antibody-based antigen; HLA-DR; CDR; antibody;
KW human leukocyte antigen; cell proliferative disorder; lymphoma;
KW MHC class II antigen disorder; lymphoma; B cell lymphoma; leukaemia;
KW acute myeloid leukaemia; rheumatoid arthritis; multiple sclerosis;
KW Grave's disease; insulin-dependent diabetes; transplant rejection;
KW systemic lupus erythematosus; graft vs. host disease; myasthenia gravis;
KW irritable bowel disease; Sjogren's syndrome; interleukin-2 secretion;
KW IL-2; MS-GPC; complementarity determining region.
XX
OS Homo sapiens.
XX
PN WO200187337-A1.
XX
PD 22-NOV-2001.
XX
PF 14-MAY-2001; 2001WO-US15625.
XX
PR 12-MAY-2000; 2000EP-0110065.
PR 06-OCT-2000; 2000US-238492P.
XX
PA (GPCB-) GPC BIOTECH AG.
PA (MORP-) MORPHOSYS AG.
XX
PI Nagy Z, Brunner C, Tesar M, Thomassen-Wolf E;
XX
DR WPI; 2002-075288/10.
XX
PT Polypeptide compositions which bind to cell surface epitopes, which in
PT multivalent form kills lymphoid tumour cells and in monovalent form
PT causes immunosuppression or inhibits activation of lymphocytes -
XX
PS Example 4; Page 66; 150pp; English.
XX
CC The invention relates to a composition which includes a polypeptide
CC or a multivalent polypeptide comprising one or more
CC antibody-based antigen -binding domain of human composition
CC with binding specificity for an antigen expressed on surface of a
CC human cell, especially HLA-DR (human leukocyte antigen DR), where
CC treating cells expressing HLA-DR with the multivalent polypeptide causes
CC or leads to killing of cells without need of cytotoxic entities or
CC immunological mechanisms. Also included are the nucleic acid
CC encoding the polypeptide, a vector comprising the nucleic acid and a host
CC cell harbouring vector or nucleic acid. The polypeptide (optionally
CC linked to cytotoxic or immunogenic agent), the nucleic acid and the host
CC cell are useful for preparing a pharmaceutical preparation for the

OM protein - protein search, using sw model

Run on: April 16, 2003, 16:56:17 ; Search time 9.51579 Seconds
(without alignments)
168.037 Million cell updates/sec

Title: US-09-644-668A-24
Perfect score: 55
Sequence: 1 RASQSVGSSYLA 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
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4	49	89.1	12	23	ABB57469	HLA-DR-specific pr
5	49	89.1	12	23	ABB57472	HLA-DR-specific pr
6	49	89.1	12	23	ABB57475	HLA-DR-specific pr
7	49	89.1	12	23	ABB57480	HLA-DR-specific pr
8	49	89.1	12	23	AAU70331	Human Kappa III li
9	49	89.1	101	23	ABB07181	CB2iE12 kappa chai
10	49	89.1	108	21	AAY53774	VL component of an
11	49	89.1	108	22	AAE08819	Human scFV L19 ant
12	49	89.1	108	23	AAO21549	Antibody screening
13	49	89.1	109	20	AAW84096	Human V kappa subg
14	49	89.1	109	22	AAB62768	Human HIV-1 monocl
15	49	89.1	109	23	ABB07231	Anti-IL-4 receptor
16	49	89.1	109	23	ABB07233	Anti-IL-4 and IL-1
17	49	89.1	110	18	AAW27545	Human Ab light cha
18	49	89.1	110	23	AAU83804	MS-GPC-6 light cha
19	49	89.1	110	23	ABB57554	HLA-DR-specific pr
20	49	89.1	110	23	ABB57556	HLA-DR-specific pr
21	49	89.1	110	23	ABB57558	HLA-DR-specific pr
22	49	89.1	110	23	ABB57562	HLA-DR-specific pr
23	49	89.1	116	14	AAR38650	Human V-kappa frag
24	49	89.1	116	15	AAR62930	Human V-kappa vk65
25	49	89.1	116	17	AAW03948	DNA fragment vk65.
26	49	89.1	116	18	AAW41146	Human vkappa65.8 f
27	49	89.1	116	19	AAW62184	Human DNA vkappa65
28	49	89.1	116	20	AAY40431	Amino acid sequenc
29	49	89.1	129	14	AAR38672	vk325-Jk2. Homo s
30	49	89.1	150	19	AAW40069	Human monoclonal a
31	49	89.1	150	22	AAE00946	Human monoclonal a
32	49	89.1	224	22	AAB99375	Human interleukin
33	49	89.1	224	22	AAB99377	Human interleukin
34	49	89.1	224	22	AAB99392	Human interleukin
35	49	89.1	224	22	AAB75008	Anti-IL8 monoclona
36	49	89.1	224	22	AAB75010	Anti-IL8 monoclona
37	49	89.1	224	22	AAB75025	Anti-IL8 monoclona
38	49	89.1	226	22	AAB99374	Human interleukin
39	49	89.1	226	22	AAB99376	Human interleukin
40	49	89.1	226	22	AAB99378	Human interleukin
41	49	89.1	226	22	AAB99394	Human interleukin
42	49	89.1	226	22	AAB99397	Human interleukin
43	49	89.1	226	22	AAB75007	Anti-IL8 monoclona
44	49	89.1	226	22	AAB75009	Anti-IL8 monoclona
45	49	89.1	226	22	AAB75011	Anti-IL8 monoclona

ALIGNMENTS

RESULT 1
AAB67493
ID AAB67493 standard; peptide; 12 AA.
XX
AC AAB67493;
XX
DT 29-MAY-2001 (first entry)
XX
DE Human light chain complementarity determining region 1 (CDR1).
XX
KW Complementarity determining region; CDR; immune response; antibody;
KW cytotoxic T lymphocyte associated antigen-4; CTLA-4; B7 ligand; cancer;
KW autoimmune disease; infectious disease; inflammation; allergy;
KW rheumatoid arthritis; myasthenia gravis; lupus erythematosus;
KW multiple sclerosis; insulin-dependent diabetes mellitus; inflammation;
KW transplant rejection; graft versus host disease.
XX
OS Homo sapiens.
XX
PN WO200114424-A2.
XX
PD 01-MAR-2001.
XX
PF 24-AUG-2000; 2000WO-US23356.
XX
PR 24-AUG-1999; 99US-0150452.
XX
PA (MEDA-) MEDAREX INC.
XX
PI Korman AJ, Halk EL, Lonberg N;
XX
DR WPI; 2001-202933/20.
XX

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RESULT 2
Q9UL78
ID   Q9UL78      PRELIMINARY;      PRT;   109 AA.
AC   Q9UL78;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Myosin-reactive immunoglobulin light chain variable region
DE   (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98277139; PubMed=9614934;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   etus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
DR   EMBL; AF035036; AAD56272.1; -.
DR   HSSP; P80362; 1WTL.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER       1       1
FT   NON_TER     109     109
SQ   SEQUENCE   109 AA;  11646 MW;  5F675C52EC7EE197 CRC64;

  Query Match             89.1%;  Score 49;  DB 4;  Length 109;
  Best Local Similarity   91.7%;  Pred. No. 0.029;
  Matches   11;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 RASQSVGSSYLA 12
           |||||| |||||
Db      24 RASQSVSSSYLA 35


RESULT 3
P96258
ID   P96258      PRELIMINARY;      PRT;   439 AA.
AC   P96258;
DT   01-MAY-1997 (TrEMBLrel. 03, Created)
DT   01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Hypothetical protein Rv0412c.
GN   RV0412C OR MT0425 OR MTCY22G10.08C.
OS   Mycobacterium tuberculosis.
OC   Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC   Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX   NCBI_TaxID=1773;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=H37RV;
RX   MEDLINE=98295987; PubMed=9634230;
RA   Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA   Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,
RA   Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA   Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
RA   Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
RA   Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA   Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
RA   Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
RT   "Deciphering the biology of Mycobacterium tuberculosis from the
RT   complete genome sequence.";
RL   Nature 393:537-544(1998).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CDC 1551 / OSHKOSH;
RA   Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA   Peterson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E.,
RA   Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,
RA   Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
RA   Bishai W.;
RT   "Whole genome comparison of Mycobacterium tuberculosis clinical and
RT   laboratory strains.";
RL   Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; Z84724; CAB06582.1; -.
DR   EMBL; AE006946; AAK44649.1; -.
DR   TIGR; MT0425; -.
DR   TubercuList; Rv0412c; -.
KW   Hypothetical protein; Complete proteome.
FT   CONFLICT    355    355       D -> Y (IN REF. 2).
SQ   SEQUENCE   439 AA;  47115 MW;  7B57FA98C0472465 CRC64;

  Query Match             69.1%;  Score 38;  DB 16;  Length 439;
  Best Local Similarity   66.7%;  Pred. No. 25;
  Matches    8;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 RASQSVGSSYLA 12
           ||   ||||||:
Db     159 RAGNPVGSSYLS 170


RESULT 4
Q9B076
ID   Q9B076      PRELIMINARY;      PRT;   261 AA.
AC   Q9B076;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Gp45.
GN   45.
OS   Mycobacteriophage Bxb1.
OC   Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
OX   NCBI_TaxID=148603;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20572070; PubMed=11123671;
RA   Mediavilla J., Jain S., Kriakov J., Ford M.E., Duda R.L., Jacobs W.R.,
RA   Hendrix R.W., Hatfull G.F.;
RT   "Genome organization and characterization of mycobacteriophage bxb1.";
RL   Mol. Microbiol. 38:955-970(2000).
DR   EMBL; AF271693; AAG59750.1; -.
SQ   SEQUENCE   261 AA;  28704 MW;  160F6385FE4538A5 CRC64;

  Query Match             67.3%;  Score 37;  DB 9;  Length 261;
  Best Local Similarity   54.5%;  Pred. No. 22;
  Matches    6;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 RASQSVGSSYL 11
           :|::|:|:|||
Db      10 KAARSIGNSYL 20


RESULT 5
Q9BLB1
ID   Q9BLB1      PRELIMINARY;      PRT;  2311 AA.
AC   Q9BLB1;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   L5178.1.
GN   L5178.1.
OS   Leishmania major.
OC   Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX   NCBI_TaxID=5664;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=FRIEDLIN;
RA   Myler P.J., Sisk E., Cawthra J., Handley F., Vogt C., Robertson L.,
RA   McDonagh P., Stuart K., Ivens A., Worthey E.A.;
RL   Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
```

OM protein - protein search, using sw model

Run on: April 16, 2003, 17:13:59 ; Search time 12.2947 Seconds
(without alignments)
201.108 Million cell updates/sec

Title: US-09-644-668A-24
Perfect score: 55
Sequence: 1 RASQSVGSSYLA 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_21:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	49	89.1	109	4	Q9UL86	Q9ul86 homo sapien
2	49	89.1	109	4	Q9UL78	Q9ul78 homo sapien
3	38	69.1	439	16	P96258	P96258 mycobacteri
4	37	67.3	261	9	Q9B076	Q9b076 mycobacteri
5	36	65.5	2311	5	Q9BLB1	Q9blb1 leishmania
6	35	63.6	316	16	Q98K17	Q98k17 rhizobium l
7	35	63.6	378	16	Q9A6C2	Q9a6c2 caulobacter
8	35	63.6	387	16	Q985D0	Q985d0 rhizobium l
9	35	63.6	387	16	Q92VK1	Q92vk1 rhizobium m
10	35	63.6	393	16	Q8Y2Q6	Q8y2q6 ralstonia s
11	35	63.6	823	5	Q9XXS6	Q9xxs6 caenorhabdi
12	35	63.6	2179	12	Q91DM0	Q91dm0 petunia vei
13	34	61.8	158	11	Q8R4K6	Q8r4k6 rattus norv
14	34	61.8	204	2	Q93NF6	Q93nf6 arthrobacte
15	34	61.8	339	5	O17844	O17844 caenorhabdi
16	34	61.8	382	16	Q8YEF5	Q8yef5 brucella me
17	34	61.8	401	10	Q9FS87	Q9fs87 solanum t
18	34	61.8	408	10	Q9SM62	Q9sm62 pisum sati
19	34	61.8	409	10	Q9SM61	Q9sm61 pisum sativ
20	34	61.8	421	16	Q8UA97	Q8ua97 agrobacteri
21	34	61.8	464	17	Q97AJ5	Q97aj5 thermoplasm
22	34	61.8	595	17	Q8TRN3	Q8trn3 methanosarc
23	34	61.8	611	16	Q9PPW9	Q9ppw9 ureaplasma
24	34	61.8	716	16	Q98JS7	Q98js7 rhizobium l
25	34	61.8	782	4	Q96A82	Q96a82 homo sapien
26	34	61.8	863	12	Q87027	Q87027 saccharomyc
27	34	61.8	1055	10	Q9SVF0	Q9svf0 arabidopsis
28	33.5	60.9	107	4	Q96SA9	Q96sa9 homo sapien
29	33.5	60.9	108	4	Q9UL77	Q9ul77 homo sapien
30	33	60.0	152	16	Q98NC2	Q98nc2 rhizobium l
31	33	60.0	259	10	Q38730	Q38730 arum macula
32	33	60.0	282	10	Q8S7V3	Q8s7v3 oryza sativ
33	33	60.0	315	16	Q99WQ0	Q99wq0 staphylococ
34	33	60.0	363	16	Q8XK57	Q8xk57 clostridium
35	33	60.0	387	2	Q9R9S5	Q9r9s5 aeromonas p
36	33	60.0	403	2	Q9ZBL6	Q9zbl6 mycobacteri
37	33	60.0	405	5	Q95YR0	Q95yr0 leishmania
38	33	60.0	432	17	Q96YG4	Q96yg4 sulfolobus
39	33	60.0	442	16	Q9CEG6	Q9ceg6 lactococcus
40	33	60.0	446	5	Q9N3X0	Q9n3x0 caenorhabdi
41	33	60.0	469	12	Q9PZG0	Q9pzg0 influenza a
42	33	60.0	474	10	Q9XEE9	Q9xee9 arabidopsis
43	33	60.0	569	3	Q96UA2	Q96ua2 neurospora
44	33	60.0	693	17	O58898	O58898 pyrococcus
45	33	60.0	894	5	Q9I7Q0	Q9i7q0 drosophila

ALIGNMENTS

RESULT 1
Q9UL86
ID Q9UL86 PRELIMINARY; PRT; 109 AA.
AC Q9UL86;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Myosin-reactive immunoglobulin kappa chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035028; AAD56264.1; -.
DR HSSP; P80362; 1WTL.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGv; 1.
FT NON_TER 1 1
FT NON_TER 109 109
SQ SEQUENCE 109 AA; 11928 MW; 243325F72C7DAC83 CRC64;

Query Match 89.1%; Score 49; DB 4; Length 109;
Best Local Similarity 91.7%; Pred. No. 0.029;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy       1 RASQSVGSSYLA 12
           |||||| |||||
Db      24 RASQSVSSSYLA 35
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RP   SEQUENCE FROM N.A.
RX   MEDLINE=88171307; PubMed=3127527;
RA   Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;
RT   "Autoantibody-associated kappa light chain variable region gene
RT   expressed in chronic lymphocytic leukemia with little or no somatic
RT   mutation. Implications for etiology and immunotherapy.";
RL   J. Exp. Med. 167:840-852(1988).
CC   -!- DISEASE: THE PROTEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN M
CC       AUTOANTIBODIES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCYTIC
CC       LEUKEMIA.
DR   PIR; PL0022; K3HUHA.
DR   HSSP; P80362; 1WTL.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL       1     20
FT   CHAIN       21    129       IG KAPPA CHAIN V-III REGION HAH.
FT   DOMAIN      21     43       FRAMEWORK-1.
FT   DOMAIN      44     55       COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN      56     70       FRAMEWORK-2.
FT   DOMAIN      71     77       COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN      78    109       FRAMEWORK-3.
FT   DOMAIN     110    118       COMPLEMENTARITY-DETERMINING-3.
FT   DOMAIN     119    129       JK1 SEGMENT.
FT   DISULFID    43    109       BY SIMILARITY.
FT   NON_TER    129    129
SQ   SEQUENCE   129 AA;  14073 MW;  D3C55292772774D0 CRC64;

  Query Match             89.1%;  Score 49;  DB 1;  Length 129;
  Best Local Similarity   91.7%;  Pred. No. 0.006;
  Matches   11;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 RASQSVGSSYLA 12
           |||||| |||||
Db      44 RASQSVSSSYLA 55


RESULT 3
KV3M_HUMAN
ID   KV3M_HUMAN     STANDARD;      PRT;   129 AA.
AC   P18136;
DT   01-NOV-1990 (Rel. 16, Created)
DT   01-NOV-1990 (Rel. 16, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-III region HIC precursor.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=88171307; PubMed=3127527;
RA   Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;
RT   "Autoantibody-associated kappa light chain variable region gene
RT   expressed in chronic lymphocytic leukemia with little or no somatic
RT   mutation. Implications for etiology and immunotherapy.";
RL   J. Exp. Med. 167:840-852(1988).
CC   -!- DISEASE: THE PROTEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN M
CC       AUTOANTIBODIES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCYTIC
CC       LEUKEMIA.
DR   PIR; PL0021; K3HUHI.
DR   HSSP; P80362; 1WTL.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL       1     20
FT   CHAIN       21    129       IG KAPPA CHAIN V-III REGION HIC.
FT   DOMAIN      21     43       FRAMEWORK-1.
FT   DOMAIN      44     55       COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN      56     70       FRAMEWORK-2.
FT   DOMAIN      71     77       COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN      78    109       FRAMEWORK-3.
FT   DOMAIN     110    118       COMPLEMENTARITY-DETERMINING-3.
FT   DOMAIN     119    129       JK1 SEGMENT.
FT   DISULFID    43    109       BY SIMILARITY.
FT   NON_TER    129    129
SQ   SEQUENCE   129 AA;  14070 MW;  7395528EA2BB74D6 CRC64;

  Query Match             89.1%;  Score 49;  DB 1;  Length 129;
  Best Local Similarity   91.7%;  Pred. No. 0.006;
  Matches   11;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 RASQSVGSSYLA 12
           |||||| |||||
Db      44 RASQSVSSSYLA 55


RESULT 4
KV3B_HUMAN
ID   KV3B_HUMAN     STANDARD;      PRT;   109 AA.
AC   P01620;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-III region SIE.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=82046598; PubMed=6794615;
RA   Andrews D.W., Capra J.D.;
RT   "Amino acid sequence of the variable regions of light chains from two
RT   idiotypically cross-reactive human IgM anti-gamma-globulins of the Wa
RT   group.";
RL   Biochemistry 20:5816-5822(1981).
CC   -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
CC       GLOBULIN ACTIVITY.
DR   PIR; A01892; K3HUSI.
DR   HSSP; P80362; 1WTL.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region.
FT   DISULFID     23     89       BY SIMILARITY.
FT   NON_TER     109    109
SQ   SEQUENCE   109 AA;  11775 MW;  7689C3ECD646FFB4 CRC64;

  Query Match             83.6%;  Score 46;  DB 1;  Length 109;
  Best Local Similarity   83.3%;  Pred. No. 0.021;
  Matches   10;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 RASQSVGSSYLA 12
           |||||| :||||
Db      24 RASQSVSNSYLA 35


RESULT 5
KV3F_HUMAN
ID   KV3F_HUMAN     STANDARD;      PRT;   109 AA.
AC   P01624;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Ig kappa chain V-III region POM.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
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GenCore version 5.1.4_p5_4578

OM protein - protein search, using sw model

Run on: April 16, 2003, 16:57:42 ; Search time 2.35789 Seconds
(without alignments)
211.085 Million cell updates/sec

Title: US-09-644-668A-24
Perfect score: 55
Sequence: 1 RASQSVGSSYLA 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	49	89.1	100	1	KV3C_HUMAN	P01621 homo sapien
2	49	89.1	129	1	KV3L_HUMAN	P18135 homo sapien
3	49	89.1	129	1	KV3M_HUMAN	P18136 homo sapien
4	46	83.6	109	1	KV3B_HUMAN	P01620 homo sapien
5	45	81.8	109	1	KV3F_HUMAN	P01624 homo sapien
6	45	81.8	116	1	KV3J_HUMAN	P04434 homo sapien
7	42	76.4	109	1	KV3D_HUMAN	P01622 homo sapien
8	41	74.5	109	1	KV3E_HUMAN	P01623 homo sapien
9	39	70.9	108	1	KV3A_HUMAN	P01619 homo sapien
10	38.5	70.0	115	1	KV3I_HUMAN	P04433 homo sapien
11	36	65.5	115	1	KV5I_MOUSE	P01642 mus musculu
12	35	63.6	129	1	KV4A_MOUSE	P01680 mus musculu
13	35	63.6	130	1	KV5G_MOUSE	P01639 mus musculu
14	34.5	62.7	108	1	KV1H_HUMAN	P01600 homo sapien
15	34	61.8	167	1	MBP_CAVPO	P25188 cavia porce
16	34	61.8	168	1	MBP_RABIT	P25274 oryctolagus
17	34	61.8	171	1	MBP_PANTR	P06906 pan troglod
18	34	61.8	171	1	MBP_PIG	P81558 sus scrofa
19	34	61.8	194	1	MBP_RAT	P02688 rattus norv
20	34	61.8	242	1	RRPO_SCVLA	P23172 saccharomyc
21	34	61.8	304	1	MBP_HUMAN	P02686 homo sapien
22	34	61.8	447	1	G6PI_LACLA	P81181 lactococcus
23	33	60.0	934	1	KGP3_DROME	P32023 drosophila
24	33	60.0	1141	1	SRE2_HUMAN	Q12772 homo sapien
25	32.5	59.1	117	1	KV1J_HUMAN	P01602 homo sapien
26	32	58.2	97	1	7E_DICDI	P15649 dictyosteli
27	32	58.2	312	1	YCX2_CHLMO	P09754 chlamydomon
28	32	58.2	351	1	MREB_HABIN	P44474 haemophilus
29	32	58.2	424	1	IVD_RAT	P12007 rattus norv
30	32	58.2	464	1	IFE_BRALA	Q04948 branchiosto
31	32	58.2	512	1	GUAA_AERPE	Q9y933 aeropyrum p
32	32	58.2	826	1	CRAA_BACUH	Q9s597 bacillus th
33	32	58.2	1005	1	YCP1_OENBE	P31563 oenothera b
34	32	58.2	1024	1	Y075_MYCGE	P47321 mycoplasma
35	31.5	57.3	108	1	KV3V_MOUSE	P01674 mus musculu
36	31	56.4	128	1	KV3K_HUMAN	P06311 homo sapien
37	31	56.4	237	1	TRYP_ASTFL	P00765 astacus flu
38	31	56.4	275	1	TAUC_ECOLI	Q47539 escherichia
39	31	56.4	356	1	PROB_AQUAE	O67209 aquifex aeo
40	31	56.4	357	1	AROC_CHLTR	O84373 chlamydia t
41	31	56.4	423	1	IVD_HUMAN	P26440 homo sapien
42	31	56.4	440	1	DCDA_STRCO	Q9zbh5 streptomyce
43	31	56.4	449	1	G6PI_STRMU	Q9x670 streptococc
44	31	56.4	449	1	G6PI_STRPN	Q97ng0 streptococc
45	31	56.4	449	1	G6PI_STRPY	Q9a111 streptococc

ALIGNMENTS

RESULT 1
KV3C_HUMAN
ID KV3C_HUMAN STANDARD; PRT; 100 AA.
AC P01621;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region NG9 precursor (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84093600; PubMed=6419127;
RA Bentley D.L.;
RT "Most kappa immunoglobulin mRNA in human lymphocytes is homologous to
RT a small family of germ-line V genes.";
RL Nature 307:77-80(1984).
CC -!- MISCELLANEOUS: THIS GENE WAS ISOLATED FROM THE NG9/9.1 HYBRIDOMA.
DR PIR; A01894; K3HUNG.
DR HSSP; P80362; 1WTL.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGv; 1.
KW Immunoglobulin V region; Signal; Hybridoma.
FT NON_TER 1 1
FT SIGNAL <1 4
FT CHAIN 5 100 IG KAPPA CHAIN V-III REGION NG9.
FT DISULFID 27 93 BY SIMILARITY.
FT NON_TER 100 100
SQ SEQUENCE 100 AA; 10729 MW; 5D9AF363CC52632F CRC64;

Query Match 89.1%; Score 49; DB 1; Length 100;
Best Local Similarity 91.7%; Pred. No. 0.0046;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQSVGSSYLA 12
||||||.|||||
Db 28 RASQSVSSSYLA 39

RESULT 2
KV3L_HUMAN
ID KV3L_HUMAN STANDARD; PRT; 129 AA.
AC P18135;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region HAH precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]

RESULT 3
S34096
Ig kappa chain V region - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000
C;Accession: S34096
R;Wagner, S.D.; Luzzatto, L.
Eur. J. Immunol. 23, 391-397, 1993
A;Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distribute
A;Reference number: S34076; MUID:93170387; PMID:8436174
A;Accession: S34096
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-89 <WAG>
A;Cross-references: EMBL:X67180
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F; /Domain: immunoglobulin homology <IMM>

Query Match 89.1%; Score 49; DB 2; Length 89;
Best Local Similarity 91.7%; Pred. No. 0.0096;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQSVGSSYLA 12
|||||| |||||
Db 17 RASQSVSSSYLA 28

RESULT 4
S37520
Ig kappa chain V region (V-kappa 3) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: S37520
R;Klein, U.; Kueppers, R.; Rajewsky, K.
submitted to the EMBL Data Library, September 1993
A;Description: Human IgM(+)IgD(+) cells, the major B cell subset in the peripheral blood
A;Reference number: S37501
A;Accession: S37520
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-91 <KLE>
A;Cross-references: EMBL:Z26612; NID:g405682; PIDN:CAA81365.1; PID:g405683
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

y Match 89.1%; Score 49; DB 2; Length 91;
Best Local Similarity 91.7%; Pred. No. 0.0099;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQSVGSSYLA 12
|||||| |||||
Db 7 RASQSVSSSYLA 18

RESULT 5
S67940
Ig kappa chain V region, subgroup III (clone MH52) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 19-Mar-1997 #sequence_revision 09-May-1997 #text_change 20-Mar-1998
C;Accession: S67940
R;Hexham, J.M.; Furmaniak, J.; Pegg, C.; Burton, D.R.; Smith, B.R.
Autoimmunity 12, 135-141, 1992
A;Title: Cloning of a human autoimmune response: preparation and sequencing of a human a
A;Reference number: S67940; MUID:92314301; PMID:1617110
A;Accession: S67940
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-91 <HEX>
A;Cross-references: EMBL:X73852
C;Superfamily: immunoglobulin V region; immunoglobulin homology

Query Match 89.1%; Score 49; DB 2; Length 91;
Best Local Similarity 91.7%; Pred. No. 0.0099;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQSVGSSYLA 12
|||||| |||||
Db 5 RASQSVSSSYLA 16

RESULT 6
S37513
Ig kappa chain V region (V-kappa 3) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: S37513
R;Klein, U.; Kueppers, R.; Rajewsky, K.
submitted to the EMBL Data Library, September 1993
A;Description: Human IgM(+)IgD(+) cells, the major B cell subset in the peripheral blood
A;Reference number: S37501
A;Accession: S37513
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-92 <KLE>
A;Cross-references: EMBL:Z26598; NID:g405668; PIDN:CAA81352.1; PID:g405669
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

Query Match 89.1%; Score 49; DB 2; Length 92;
Best Local Similarity 91.7%; Pred. No. 0.01;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQSVGSSYLA 12
|||||| |||||
Db 7 RASQSVSSSYLA 18

RESULT 7
S37519
Ig kappa chain V region (V-kappa 3) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: S37519
R;Klein, U.; Kueppers, R.; Rajewsky, K.
submitted to the EMBL Data Library, September 1993
A;Description: Human IgM(+)IgD(+) cells, the major B cell subset in the peripheral blood
A;Reference number: S37501
A;Accession: S37519
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-92 <KLE>
A;Cross-references: EMBL:Z26613; NID:g405680; PIDN:CAA81366.1; PID:g405681
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

Query Match 89.1%; Score 49; DB 2; Length 92;
Best Local Similarity 91.7%; Pred. No. 0.01;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQSVGSSYLA 12
|||||| |||||
Db 7 RASQSVSSSYLA 18

RESULT 8
S37517
Ig kappa chain V region (V-kappa 3) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: S37517
R;Klein, U.; Kueppers, R.; Rajewsky, K.
submitted to the EMBL Data Library, September 1993
A;Description: Human IgM(+)IgD(+) cells, the major B cell subset in the peripheral

OM protein - protein search, using sw model

Run on: April 16, 2003, 17:11:36 ; Search time 3.70526 Seconds
(without alignments)
311.344 Million cell updates/sec

Title: US-09-644-668A-24
Perfect score: 55
Sequence: 1 RASQSVGSSYLA 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	49	89.1	83	2	I30607	Ig kappa chain V-I
2	49	89.1	87	2	S16823	Ig kappa chain V r
3	49	89.1	89	2	S34096	Ig kappa chain V r
4	49	89.1	91	2	S37520	Ig kappa chain V r
5	49	89.1	91	2	S67940	Ig kappa chain V r
6	49	89.1	92	2	S37513	Ig kappa chain V r
7	49	89.1	92	2	S37519	Ig kappa chain V r
8	49	89.1	92	2	S37517	Ig kappa chain V r
9	49	89.1	92	2	S37514	Ig kappa chain V r
10	49	89.1	92	2	S37518	Ig kappa chain V r
11	49	89.1	93	2	S37526	Ig kappa chain V r
12	49	89.1	93	2	S37528	Ig kappa chain V r
13	49	89.1	93	2	S37501	Ig kappa chain V r
14	49	89.1	96	2	A30601	Ig kappa chain V-I
15	49	89.1	100	1	K3HUNG	Ig kappa chain pre
16	49	89.1	104	2	PH0964	Ig kappa chain V r
17	49	89.1	107	2	PH0965	Ig kappa chain V r
18	49	89.1	108	2	C30608	Ig kappa chain V-I
19	49	89.1	108	2	H44151	Ig kappa chain V r
20	49	89.1	109	2	PH0963	Ig kappa chain V r
21	49	89.1	109	2	B30601	Ig kappa chain V-I
22	49	89.1	109	2	A30608	Ig kappa chain V-I
23	49	89.1	109	2	D30601	Ig kappa chain V-I
24	49	89.1	109	2	P30607	Ig kappa chain V-I
25	49	89.1	109	2	C30601	Ig kappa chain V-I
26	49	89.1	109	2	H30601	Ig kappa chain V-I
27	49	89.1	116	2	B27594	Ig kappa chain pre
28	49	89.1	121	2	S40327	Ig kappa chain - h
29	49	89.1	129	1	K3HUHA	Ig kappa chain pre
30	49	89.1	129	1	K3HUHI	Ig kappa chain pre
31	49	89.1	129	2	S46369	IG light chain var
32	49	89.1	134	2	S38643	Ig kappa chain V r
33	48	87.3	114	2	S46375	Ig kappa chain V-J
34	47	85.5	93	2	S37505	Ig kappa chain V r
35	47	85.5	109	2	G30601	Ig kappa chain V-I
36	46	83.6	47	2	B30607	Ig kappa chain V-I
37	46	83.6	62	2	I30601	Ig kappa chain V-I
38	46	83.6	92	2	S37510	Ig kappa chain V r
39	46	83.6	96	2	S45441	Ig kappa chain V r
40	46	83.6	109	1	K3HUSI	Ig kappa chain V-I
41	46	83.6	111	2	S40359	Ig kappa chain V-J
42	46	83.6	116	2	C27594	Ig kappa chain pre
43	46	83.6	116	2	S41817	Ig kappa chain V r
44	46	83.6	119	2	S41816	Ig kappa chain V r
45	45	81.8	87	2	S16843	Ig kappa chain V r

ALIGNMENTS

RESULT 1
I30607
Ig kappa chain V-III region (Wei) - human (fragments)
C;Species: Homo sapiens (man)
C;Date: 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 09-May-1997
C;Accession: I30607
R;Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; S
J. Immunol. 142, 3158-3163, 1989
A;Title: Structural and idiotypic characterization of the L chains of human IgM autoa
A;Reference number: A30601; MUID:89215279; PMID:2496160
A;Accession: I30607
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-83 <GON>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

Query Match 89.1%; Score 49; DB 2; Length 83;
Best Local Similarity 91.7%; Pred. No. 0.0089;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy       1 RASQSVGSSYLA 12
             |||||| |||||
Db      24 RASQSVSSSYLA 35
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RESULT 2
S16823
Ig kappa chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C;Accession: S16823
R;Blaison, G.; Kuntz, J.L.; Pasquali, J.L.
Eur. J. Immunol. 21, 1221-1227, 1991
A;Title: Molecular analysis of V(kappa)III variable regions of polyclonal rheumatoid
A;Reference number: S16823; MUID:91243737; PMID:1903706
A;Accession: S16823
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-87 <BLA>
A;Cross-references: EMBL:X54821
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;7-82/Domain: immunoglobulin homology <IMM>

Query Match 89.1%; Score 49; DB 2; Length 87;
Best Local Similarity 91.7%; Pred. No. 0.0094;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy       1 RASQSVGSSYLA 12
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Db      15 RASQSVSSSYLA 26
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Db      61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRKDWGW-ALFDYWGQGTLVTV 119

Qy     117 S 117
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Db     120 S 120
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RESULT 2
US-08-331-398A-46
; Sequence 46, Application US/08331398A
; Patent No. 5608039
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira
; APPLICANT: Willingham, Mark
; APPLICANT: FitzGerald, David
; APPLICANT: Brinkmann, Ulrich
; APPLICANT: Pai, Lee
; TITLE OF INVENTION: Single Chain B3 Antibody Fusion Proteins
; TITLE OF INVENTION: and Their Uses (as amended)
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/331,398A
; FILING DATE: 28-OCT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/767,331
; FILING DATE: 30-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/596,289
; FILING DATE: 12-OCT-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 015280-126110US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..119
; OTHER INFORMATION: /note= "Human fetal immunoglobulin
; OTHER INFORMATION: 56P1'CL Variable Heavy chain (V-H)"
US-08-331-398A-46

Query Match 86.7%; Score 549.5; DB 1; Length 119;
Best Local Similarity 89.1%; Pred. No. 6e-46;
Matches 106; Conservative 4; Mismatches 8; Indels 1; Gaps 1;

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Qy       1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVTFISYDGNNKYY 60
           ||:|||||||||||||||||||||||||||| |||||||||||||||  |||||:||||
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Qy      61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAIYYCA-RTGWLGPFDYWGQGTLVTVSS 118
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RESULT 3
US-08-331-397B-46
; Sequence 46, Application US/08331397B
; Patent No. 5981726
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira
; APPLICANT: Benhar, Itai
; TITLE OF INVENTION: Chimeric and Mutationally Stabilized Tumor-
; TITLE OF INVENTION: Specific Antibody Fragments, Fusion Proteins, and Uses
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/331,397B
; FILING DATE: 28-OCT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/767,331
; FILING DATE: 30-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/596,289
; FILING DATE: 12-OCT-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 015280-126120US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..119
; OTHER INFORMATION: /note= "Human fetal immunoglobulin
; OTHER INFORMATION: 56P1'CL Variable Heavy chain (V-H)"
US-08-331-397B-46

Query Match 86.7%; Score 549.5; DB 2; Length 119;
Best Local Similarity 89.1%; Pred. No. 6e-46;
Matches 106; Conservative 4; Mismatches 8; Indels 1; Gaps 1;

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           ||:|||||||||||||||||||||||||||| |||||||||||||||  |||||:||||
Db       1 QVELVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60

Qy      61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAIYYCA-RTGWLGPFDYWGQGTLVTVSS 118
           |||||||||||||||||||||||||||||||||||:|||| |:     ||||||||||||||
Db      61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARRSARTYYFDYWGQGTLVTVSS 119
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RESULT 4
US-08-759-804A-46

GenCore version 5.1.4_p5_4578

OM protein - protein search, using sw model

Run on: April 16, 2003, 17:15:40 ; Search time 30.2246 Seconds
(without alignments)
114.870 Million cell updates/sec

Title: US-09-644-668A-17
Perfect score: 634
Sequence: 1 QVQLVESGGGVVQPGRSLRL.....TGWLGPFDYWGQGTLVTVSS 118

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
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4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	558.5	88.1	120	1	US-07-942-245-35	Sequence 35, Appl
2	549.5	86.7	119	1	US-08-331-398A-46	Sequence 46, Appl
3	549.5	86.7	119	2	US-08-331-397B-46	Sequence 46, Appl
4	549.5	86.7	119	2	US-08-759-804A-46	Sequence 46, Appl
5	549.5	86.7	119	4	US-09-227-693-46	Sequence 46, Appl
6	533.5	84.1	117	4	US-09-025-769B-24	Sequence 24, Appl
7	530.5	83.7	116	1	US-08-211-202-141	Sequence 141, App
8	530.5	83.7	125	4	US-09-240-274-24	Sequence 24, Appl
9	529.5	83.5	125	4	US-09-240-274-9	Sequence 9, Appli
10	524.5	82.7	125	4	US-09-240-274-8	Sequence 8, Appli
11	524.5	82.7	125	4	US-09-240-274-20	Sequence 20, Appl
12	524.5	82.7	125	4	US-09-240-274-21	Sequence 21, Appl
13	524.5	82.7	125	4	US-09-240-274-22	Sequence 22, Appl
14	523	82.5	126	4	US-09-240-274-149	Sequence 149, App
15	520	82.0	128	4	US-09-240-274-1	Sequence 1, Appli
16	517	81.5	310	4	US-09-079-029-11	Sequence 11, Appl
17	516.5	81.5	125	4	US-09-240-274-23	Sequence 23, Appl
18	515	81.2	126	4	US-09-240-274-10	Sequence 10, Appl
19	515	81.2	126	4	US-09-240-274-144	Sequence 144, App
20	515	81.2	126	4	US-09-240-274-150	Sequence 150, App
21	514.5	81.2	113	3	US-08-974-899-6	Sequence 6, Appli
22	514	81.1	128	4	US-09-240-274-142	Sequence 142, App
23	513	80.9	122	2	US-07-934-373C-21	Sequence 21, Appl
24	513	80.9	122	3	US-08-437-642B-21	Sequence 21, Appl
25	513	80.9	122	4	US-08-146-206C-21	Sequence 21, Appl
26	513	80.9	122	5	PCT-US93-07832-21	Sequence 21, Appl
27	513	80.9	126	4	US-09-240-274-152	Sequence 152, App
28	509.5	80.4	117	4	US-09-157-370-1	Sequence 1, Appli
29	509	80.3	124	4	US-09-240-274-4	Sequence 4, Appli
30	508	80.1	120	4	US-09-025-769B-38	Sequence 38, Appl
31	508	80.1	120	4	US-09-025-769B-63	Sequence 63, Appl
32	508	80.1	141	1	US-08-259-372A-2	Sequence 2, Appli
33	508	80.1	141	1	US-08-468-671-2	Sequence 2, Appli
34	508	80.1	281	4	US-09-025-769B-178	Sequence 178, App
35	507.5	80.0	123	2	US-08-665-202-30	Sequence 30, Appl
36	507	80.0	123	4	US-08-983-607-38	Sequence 38, Appl
37	506	79.8	117	1	US-07-942-245-36	Sequence 36, Appl
38	504	79.5	131	4	US-08-983-607-28	Sequence 28, Appl
39	502.5	79.3	127	4	US-09-240-274-139	Sequence 139, App
40	502.5	79.3	129	4	US-09-240-274-143	Sequence 143, App
41	502	79.2	124	4	US-09-240-274-7	Sequence 7, Appli
42	502	79.2	459	1	US-08-157-101A-7	Sequence 7, Appli
43	501.5	79.1	127	4	US-09-240-274-18	Sequence 18, Appl
44	501	79.0	125	1	US-08-276-852-76	Sequence 76, Appl
45	501	79.0	125	1	US-08-899-575-76	Sequence 76, Appl

ALIGNMENTS

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RESULT 1
US-07-942-245-35
; Sequence 35, Application US/07942245
; Patent No. 5639641
;  GENERAL INFORMATION:
;    APPLICANT:  PEDERSEN, Jan T.
;    APPLICANT:  SEARLE,   Stephen M.J.
;    APPLICANT:  REES,     Anthony R.
;    APPLICANT:  ROGUSKA,  Michael A.
;    APPLICANT:  GUILD,    Braydon C.
;    TITLE OF INVENTION:  SURFACE RESIDUE VENEERING OF RODENT
;    TITLE OF INVENTION:  ANTIBODIES
;    NUMBER OF SEQUENCES:  522
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sughrue, Mion, Zinn, Macpeak & Seas
;      STREET:  2100 Pensylvania Avenue, N.W.
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  United States
;      ZIP:  20037-3202
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  HP 9000/700 Workstation
;      OPERATING SYSTEM:  UNIX
;      SOFTWARE:  In house
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/942,245
;      FILING DATE:  09-SEP-1992
;      CLASSIFICATION:  530
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 293-7060
;      TELEFAX:  (202) 293-7860
;      TELEX:  6491103
;  INFORMATION FOR SEQ ID NO:  35:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  120 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-07-942-245-35

  Query Match             88.1%;  Score 558.5;  DB 1;  Length 120;
  Best Local Similarity   89.3%;  Pred. No. 8.3e-47;
  Matches  108;  Conservative    2;  Mismatches    6;  Indels    5;  Gaps    2;

Qy       1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVTFISYDGNNKYY 60
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Db       1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60

Qy      61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAIYYCART----GWLGPFDYWGQGTLVTV 116
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Db    121 TVSS 124


RESULT 2
US-09-880-748-1519
; Sequence 1519, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
;  APPLICANT: Ruben et al.
;  TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
;  FILE REFERENCE: PF523
;  CURRENT APPLICATION NUMBER: US/09/880,748
;  CURRENT FILING DATE:  2001-06-15
;  PRIOR APPLICATION NUMBER: 60/212,210
;  PRIOR FILING DATE: 2000-06-15
;  PRIOR APPLICATION NUMBER: 60/240,816
;  PRIOR FILING DATE: 2000-10-17
;  PRIOR APPLICATION NUMBER: 60/276,248
;  PRIOR FILING DATE: 2001-03-16
;     OR APPLICATION NUMBER: 60/277,379
;     OR FILING DATE: 2001-03-21
;  PRIOR APPLICATION NUMBER: 60/293,499
;  PRIOR FILING DATE: 2001-05-25
;  NUMBER OF SEQ ID NOS: 3239
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1519
;    LENGTH: 252
;    TYPE: PRT
;    ORGANISM: Homo sapiens
US-09-880-748-1519

  Query Match             88.6%;  Score 562;  DB 9;  Length 252;
  Best Local Similarity   86.3%;  Pred. No. 3.5e-35;
  Matches  107;  Conservative    5;  Mismatches    6;  Indels    6;  Gaps    1;

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Db       1 QVQLQESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNKYY 60

Qy      61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAIYYCAR------TGWLGPFDYWGQGTLV 114
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Db      61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKRQYDILTGYYGGFDYWGQGTMV 120

Qy     115 TVSS 118
           ||||
Db     121 TVSS 124


RESULT 3
US-09-880-748-983
; Sequence 983, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
;  APPLICANT: Ruben et al.
;  TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
;  FILE REFERENCE: PF523
;  CURRENT APPLICATION NUMBER: US/09/880,748
;  CURRENT FILING DATE:  2001-06-15
;  PRIOR APPLICATION NUMBER: 60/212,210
;  PRIOR FILING DATE: 2000-06-15
;  PRIOR APPLICATION NUMBER: 60/240,816
;  PRIOR FILING DATE: 2000-10-17
;  PRIOR APPLICATION NUMBER: 60/276,248
;  PRIOR FILING DATE: 2001-03-16
;  PRIOR APPLICATION NUMBER: 60/277,379
;  PRIOR FILING DATE: 2001-03-21
;  PRIOR APPLICATION NUMBER: 60/293,499
;  PRIOR FILING DATE: 2001-05-25
;  NUMBER OF SEQ ID NOS: 3239
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 983
;    LENGTH: 254
;    TYPE: PRT
;    ORGANISM: Homo sapiens
US-09-880-748-983

  Query Match             88.3%;  Score 560;  DB 9;  Length 254;
  Best Local Similarity   84.4%;  Pred. No. 4.9e-35;
  Matches  108;  Conservative    5;  Mismatches    5;  Indels   10;  Gaps    2;

Qy       1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVTFISYDGNNKYY 60
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Db       1 QVQLQESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60

Qy      61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAIYYCAR--------TGWLGP--FDYWGQ 110
           ||||||||||||||||||||||||||||:|||||         ||: ||  |||||:
Db      61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAREEGFYDILTGYYGPGYFDYWGK 120

Qy     111 GTLVTVSS 118
           ||:|||||
Db     121 GTMVTVSS 128


RESULT 4
US-09-880-748-1201
; Sequence 1201, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
;  APPLICANT: Ruben et al.
;  TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
;  FILE REFERENCE: PF523
;  CURRENT APPLICATION NUMBER: US/09/880,748
;  CURRENT FILING DATE:  2001-06-15
;  PRIOR APPLICATION NUMBER: 60/212,210
;  PRIOR FILING DATE: 2000-06-15
;  PRIOR APPLICATION NUMBER: 60/240,816
;  PRIOR FILING DATE: 2000-10-17
;  PRIOR APPLICATION NUMBER: 60/276,248
;  PRIOR FILING DATE: 2001-03-16
;  PRIOR APPLICATION NUMBER: 60/277,379
;  PRIOR FILING DATE: 2001-03-21
;  PRIOR APPLICATION NUMBER: 60/293,499
;  PRIOR FILING DATE: 2001-05-25
;  NUMBER OF SEQ ID NOS: 3239
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1201
;    LENGTH: 252
;    TYPE: PRT
;    ORGANISM: Homo sapiens
US-09-880-748-1201

  Query Match             87.9%;  Score 557;  DB 9;  Length 252;
  Best Local Similarity   85.5%;  Pred. No. 8.2e-35;
  Matches  106;  Conservative    6;  Mismatches    6;  Indels    6;  Gaps    1;

Qy       1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVTFISYDGNNKYY 60
           |:|| |||||||||||||||||||||||| ||||||||||||||  |||||:||||
Db       1 QLQLQESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNKYY 60

Qy      61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAIYYCAR------TGWLGPFDYWGQGTLV 114
           ||||||||||||||||||||||||||||:||||:      ||: | |||||:||||
Db      61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKRQYDILTGYYGGFDYWGKGTLV 120

Qy     115 TVSS 118
           ||||
Db     121 TVSS 124


RESULT 5
US-09-880-748-1627
; Sequence 1627, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
;  APPLICANT: Ruben et al.
;  TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
;  FILE REFERENCE: PF523
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GenCore version 5.1.4_p5_4578

OM protein - protein search, using sw model

Run on: April 16, 2003, 17:21:54 ; Search time 34.7789 Seconds
(without alignments)
256.547 Million cell updates/sec

Title: US-09-644-668A-17
Perfect score: 634
Sequence: 1 QVQLVESGGGVVQPGRSLRL.....TGWLGPFDYWGQGTLVTVSS 118

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 288829 seqs, 75613885 residues

Total number of hits satisfying chosen parameters: 288829

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
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2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
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4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	570	89.9	247	9	US-09-880-748-924	Sequence 924, App
2	562	88.6	252	9	US-09-880-748-1519	Sequence 1519, Ap
3	560	88.3	254	9	US-09-880-748-983	Sequence 983, App
4	557	87.9	252	9	US-09-880-748-1201	Sequence 1201, Ap
5	550	86.8	252	9	US-09-880-748-1627	Sequence 1627, Ap
6	549	86.6	249	9	US-09-880-748-1109	Sequence 1109, Ap
7	546.5	86.2	248	9	US-09-880-748-1421	Sequence 1421, Ap
8	541.5	85.4	241	9	US-09-880-748-2055	Sequence 2055, Ap
9	541	85.3	253	9	US-09-880-748-1200	Sequence 1200, Ap
10	540	85.2	252	9	US-09-880-748-956	Sequence 956, App
11	539	85.0	249	9	US-09-880-748-512	Sequence 512, App
12	537	84.7	254	9	US-09-880-748-977	Sequence 977, App
13	535.5	84.5	252	9	US-09-880-748-1731	Sequence 1731, Ap
14	534	84.2	254	9	US-09-880-748-881	Sequence 881, App
15	532	83.9	244	9	US-09-880-748-1910	Sequence 1910, Ap
16	532	83.9	247	9	US-09-880-748-1330	Sequence 1330, Ap
17	530.5	83.7	125	9	US-09-848-798-24	Sequence 24, Appl
18	529.5	83.5	125	9	US-09-848-798-9	Sequence 9, Appli
19	529.5	83.5	240	9	US-09-880-748-1898	Sequence 1898, Ap
20	528	83.3	254	9	US-09-880-748-1759	Sequence 1759, Ap
21	527.5	83.2	252	9	US-09-880-748-988	Sequence 988, App
22	527.5	83.2	252	9	US-09-880-748-1394	Sequence 1394, Ap
23	526	83.0	251	9	US-09-880-748-952	Sequence 952, App
24	526	83.0	251	9	US-09-880-748-982	Sequence 982, App
25	526	83.0	251	9	US-09-880-748-1512	Sequence 1512, Ap
26	526	83.0	251	9	US-09-880-748-1554	Sequence 1554, Ap
27	525.5	82.9	251	9	US-09-880-748-955	Sequence 955, App
28	525	82.8	122	9	US-09-144-886-69	Sequence 69, Appl
29	525	82.8	241	9	US-09-880-748-1887	Sequence 1887, Ap
30	525	82.8	241	9	US-09-880-748-1901	Sequence 1901, Ap
31	525	82.8	248	9	US-09-880-748-1890	Sequence 1890, Ap
32	525	82.8	249	9	US-09-880-748-397	Sequence 397, App
33	525	82.8	249	9	US-09-880-748-1102	Sequence 1102, Ap
34	525	82.8	249	9	US-09-880-748-1115	Sequence 1115, Ap
35	525	82.8	254	9	US-09-880-748-981	Sequence 981, App
36	524.5	82.7	125	9	US-09-848-798-8	Sequence 8, Appli
37	524.5	82.7	125	9	US-09-848-798-20	Sequence 20, Appl
38	524.5	82.7	125	9	US-09-848-798-21	Sequence 21, Appl
39	524.5	82.7	125	9	US-09-848-798-22	Sequence 22, Appl
40	524.5	82.7	249	9	US-09-880-748-912	Sequence 912, App
41	524	82.6	249	9	US-09-880-748-1724	Sequence 1724, Ap
42	524	82.6	249	9	US-09-880-748-1725	Sequence 1725, Ap
43	523	82.5	122	9	US-09-144-886-68	Sequence 68, Appl
44	523	82.5	126	9	US-09-848-798-149	Sequence 149, App
45	523	82.5	239	9	US-09-880-748-1882	Sequence 1882, Ap

ALIGNMENTS

RESULT 1
US-09-880-748-924
; Sequence 924, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 924
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-924

Query Match 89.9%; Score 570; DB 9; Length 247;
Best Local Similarity 88.7%; Pred. No. 8.6e-36;
Matches 110; Conservative 3; Mismatches 5; Indels 6; Gaps 1;

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Qy      61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAIYYCAR------TGWLGPFDYWGQGTLV 114
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Qy     115 TVSS 118
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GenCore version 5.1.4_p5_4578

OM protein - protein search, using sw model

Run on: April 16, 2003, 16:56:17 ; Search time 93.5719 Seconds
(without alignments)
168.037 Million cell updates/sec

Title: US-09-644-668A-17
Perfect score: 634
Sequence: 1 QVQLVESGGGVVQPGRSLRL.....TGWLGPFDYWGQGTLVTVSS 118

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	634	100.0	118	22	AAB67508	Light chain variab
2	634	100.0	118	22	AAB67513	Heavy chain variab
3	623	98.3	118	22	AAB67509	Light chain variab
4	623	98.3	118	22	AAB67514	Heavy chain variab
5	570	89.9	247	23	ABP44913	Human BLyS binding
6	566.5	89.4	225	22	AAB99369	Human interleukin
7	566.5	89.4	225	22	AAB99380	Human interleukin
8	566.5	89.4	225	22	AAB75002	Anti-IL8 monoclona
9	566.5	89.4	225	22	AAB75013	Anti-IL8 monoclona
10	564	89.0	463	21	AAY93701	The heavy chain of
11	564	89.0	463	21	AAY93727	The heavy chain of
12	564	89.0	463	21	AAY93728	The heavy chain of
13	562	88.6	252	23	ABP45508	Human BLyS binding
14	561.5	88.6	225	22	AAB99388	Human interleukin
15	561.5	88.6	225	22	AAB75021	Anti-IL8 monoclona
16	560.5	88.4	225	22	AAB99387	Human interleukin
17	560.5	88.4	225	22	AAB75020	Anti-IL8 monoclona
18	560	88.3	254	23	ABP44972	Human BLyS binding
19	558.5	88.1	120	15	AAR52064	Heavy chain variab
20	558.5	88.1	225	22	AAB99367	Human interleukin
21	558.5	88.1	225	22	AAB75000	Anti-IL8 monoclona
22	558	88.0	463	21	AAY93707	The heavy chain of
23	558	88.0	463	21	AAY93732	The heavy chain of
24	557.5	87.9	119	22	AAU02515	Anti-adipocyte mon
25	557	87.9	252	23	ABP45190	Human BLyS binding
26	555.5	87.6	519	23	AAU81993	Human secreted pro
27	554.5	87.5	225	22	AAB99389	Human interleukin
28	554.5	87.5	225	22	AAB75022	Anti-IL8 monoclona
29	554	87.4	118	23	ABB07230	Anti-IL-4 receptor
30	554	87.4	254	21	AAY56287	HCAT1 clone 25 ant
31	554	87.4	490	21	AAY56637	hCAT1 binding huma
32	552.5	87.1	225	22	AAB99381	Human interleukin
33	552.5	87.1	225	22	AAB99385	Human interleukin
34	552.5	87.1	225	22	AAB75014	Anti-IL8 monoclona
35	552.5	87.1	225	22	AAB75018	Anti-IL8 monoclona
36	551.5	87.0	115	21	AAB39519	Anti-IL12 antibody
37	550	86.8	252	23	ABP45616	Human BLyS binding
38	549.5	86.7	119	17	AAR95216	Human foetal immun
39	549	86.6	118	23	ABG30463	Human anti-CD40 mo
40	549	86.6	249	23	ABP45098	Human BLyS binding
41	547.5	86.4	119	22	AAB67516	Heavy chain variab
42	547	86.3	137	23	ABB77063	ACZ885 antibody he
43	546.5	86.2	248	23	ABP45410	Human BLyS binding
44	546	86.1	122	22	AAB72883	Human anti-HER2/ne
45	545	86.0	223	20	AAY08598	Anti-human TNF-alp

ALIGNMENTS

RESULT 1
AAB67508
ID AAB67508 standard; peptide; 118 AA.
XX
AC AAB67508;
XX
DT 29-MAY-2001 (first entry)
XX
DE Light chain variable region of anti-CTLA-4 antibody 10D1.
XX
KW Complementarity determining region; CDR; immune response; antibody;
KW cytotoxic T lymphocyte associated antigen-4; CTLA-4; B7 ligand; cancer;
KW autoimmune disease; infectious disease; inflammation; allergy;
KW rheumatoid arthritis; myasthenia gravis; lupus erythematosus;
KW multiple sclerosis; insulin-dependent diabetes mellitus; inflammation;
KW transplant rejection; graft versus host disease.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
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FT /note= "CDR1"
FT Region 50..66
FT /note= "CDR2"
FT Region 99..107
FT /note= "CDR3"
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PN WO200114424-A2.
XX
PD 01-MAR-2001.
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PF 24-AUG-2000; 2000WO-US23356.
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Qy      62 DSVKGRFTISRDNSKNTLYLQMNSLRAEDTAIYYCARTGWLGPFDYWGQGTLVTVSS 118
           ||||||||||||||||||||||||||||||:||||  | ||  ||||||||||||
Db      61 DSVKGRFTISRDNSKNTLYLQMNSLRAEDTAMYYCAGGGGLG-LGYWGQGTLVTVSS 116


RESULT 2
Q8WUK1
ID   Q8WUK1      PRELIMINARY;      PRT;   613 AA.
AC   Q8WUK1;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Hypothetical 67.3 kDa protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC    TISSUE=TONSIL;
RA    crausberg R.;
RL   Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC020240; AAH20240.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 5.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 4.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_3.
KW   Hypothetical protein.
SQ   SEQUENCE   613 AA;  67296 MW;  60C7F5950671E315 CRC64;

  Query Match             85.6%;  Score 543;  DB 4;  Length 613;
  Best Local Similarity   86.8%;  Pred. No. 1.6e-46;
  Matches  105;  Conservative    5;  Mismatches    7;  Indels    4;  Gaps    2;

Qy       1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVTFISYDGNNKYY 60
           |||||||||||||||||||||||||||||| ||||||||||||||  |||||:||||
Db      20 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNKYY 79

Qy      61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAIYYCARTGW---LGPFDYWGQGTLVTVS 117
           |||||||||||||||||||||||||||||:||||:  |   :  || |||||:||||
Db      80 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAK-DWSEGVETFDIWGQGTMVTVS 138

Qy     118 S 118
           |
Db     139 S 139


RESULT 3
Q9UL90
ID   Q9UL90      PRELIMINARY;      PRT;   113 AA.
AC   Q9UL90;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Myosin-reactive immunoglobulin heavy chain variable region
DE   (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98277139; PubMed=9614934;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
DR   EMBL; AF035024; AAD56260.1; -.
DR   HSSP; P01772; 2FB4.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER       1      1
FT   NON_TER     113    113
SQ   SEQUENCE   113 AA;  12437 MW;  ED57FDD19086D07F CRC64;

  Query Match             84.3%;  Score 534.5;  DB 4;  Length 113;
  Best Local Similarity   86.4%;  Pred. No. 1.5e-46;
  Matches  102;  Conservative    5;  Mismatches    6;  Indels    5;  Gaps    1;

Qy       1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVTFISYDGNNKYY 60
           :|||||||||||||| |||||||||||||| |||||||||||||| || |||:||||
Db       1 EVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIRYDGSNKYY 60

Qy      61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAIYYCARTGWLGPFDYWGQGTLVTVSS 118
           ||||||||||||||||||||||||||||||:||||:       :||||||||||||
Db      61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAK-----DLNYWGQGTLVTVSS 113


RESULT 4
Q9Y509
ID   Q9Y509      PRELIMINARY;      PRT;   147 AA.
AC   Q9Y509;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   VH3 protein (Fragment).
GN   VH3.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96071149; PubMed=7475288;
RA   Cao J., Vescio R.A., Rettig M.B., Hong C.H., Kim A., Lee J.C.,
RA   Lichtenstein A.K., Berenson J.R.;
RT   "A CD10-positive subset of malignant cells is identified in multiple
RT   myeloma using PCR with patient-specific immunoglobulin gene primers.";
RL   Leukemia 9:1948-1953(1995).
DR   EMBL; S80860; AAD14339.1; -.
DR   HSSP; P01772; 2FB4.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER       1      1
SQ   SEQUENCE   147 AA;  15768 MW;  8489FCAAA7BC925C CRC64;

  Query Match             78.4%;  Score 497;  DB 4;  Length 147;
  Best Local Similarity   75.4%;  Pred. No. 1.2e-42;
  Matches   95;  Conservative    8;  Mismatches   15;  Indels    8;  Gaps    1;

Qy       1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVTFISYDGNNKYY 60
           || |||||||||||:|||||| |||||||:| | ||||||||||:||  |||||: :||
Db       1 QVHLVESGGGVVQPGKSLRLSCEASGFTFSTYGMSWVRQAPGKGLDWVALISYDGSTQYY 60

Qy      61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAIYYCARTG--------WLGPFDYWGQGT 112
           | ||||||||||||||||||| ||| |||||:||||: |         :    |||||||
Db      61 AGSVKGRFTISRDNSKNTLYLQMTSLRVEDTAVYYCAKDGNYFDSVGYYYAGIDYWGQGT 120

Qy     113 LVTVSS 118
           ||||||
Db     121 LVTVSS 126


RESULT 5
Q9UL84
ID   Q9UL84      PRELIMINARY;      PRT;   122 AA.
```

GenCore version 5.1.4_p5_4578

OM protein - protein search, using sw model

Run on: April 16, 2003, 17:13:59 ; Search time 120.898 Seconds
(without alignments)
201.108 Million cell updates/sec

Title: US-09-644-668A-17
Perfect score: 634
Sequence: 1 QVQLVESGGGVVQPGRSLRL.....TGWLGPFDYWGQGTLVTVSS 118

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_21:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	546.5	86.2	116	4	Q9UL93	Q9ul93 homo sapien
2	543	85.6	613	4	Q8WUK1	Q8wuk1 homo sapien
3	534.5	84.3	113	4	Q9UL90	Q9ul90 homo sapien
4	497	78.4	147	4	Q9Y509	Q9y509 homo sapien
5	496	78.2	122	4	Q9UL84	Q9ul84 homo sapien
6	494.5	78.0	121	4	Q9UL71	Q9ul71 homo sapien
7	482	76.0	118	4	Q9UL91	Q9ul91 homo sapien
8	481.5	75.9	597	4	Q96BB9	Q96bb9 homo sapien
9	478	75.4	573	4	Q8WU38	Q8wu38 homo sapien
10	474	74.8	471	4	Q8TC77	Q8tc77 homo sapien
11	469	74.0	118	4	Q9UL72	Q9ul72 homo sapien
12	469	74.0	473	11	Q91Z05	Q91z05 mus musculu
13	458	72.2	112	4	Q9HCC1	Q9hcc1 homo sapien
14	449	70.8	494	4	Q96K68	Q96k68 homo sapien
15	438.5	69.2	119	11	Q920E7	Q920e7 mus musculu
16	438	69.1	487	11	Q99KA4	Q99ka4 mus musculu
17	430.5	67.9	479	11	Q91WP5	Q91wp5 mus musculu
18	423	66.7	95	4	Q9ULB6	Q9ulb6 homo sapien
19	412.5	65.1	131	4	Q9UL88	Q9ul88 homo sapien
20	405	63.9	469	11	Q8R3V9	Q8r3v9 mus musculu
21	400	63.1	298	11	Q9QYF0	Q9qyf0 mus musculu
22	394	62.1	484	11	Q8VEA0	Q8vea0 mus musculu
23	392.5	61.9	104	4	Q9UL87	Q9ul87 homo sapien
24	391.5	61.8	486	11	Q91Z07	Q91z07 mus musculu
25	386	60.9	124	4	Q9UL92	Q9ul92 homo sapien
26	384.5	60.6	480	11	Q91XE1	Q91xe1 mus musculu
27	382	60.3	437	11	Q9R1A4	Q9r1a4 mus musculu
28	370.5	58.4	112	4	Q9UGP3	Q9ugp3 homo sapien
29	356.5	56.2	125	4	Q9UL95	Q9ul95 homo sapien
30	354.5	55.9	484	11	Q99LA6	Q99la6 mus musculu
31	352.5	55.6	119	4	Q9UL94	Q9ul94 homo sapien
32	351	55.4	124	6	Q9N0W4	Q9n0w4 oryctolagus
33	348	54.9	124	6	Q9N0W6	Q9n0w6 oryctolagus
34	344.5	54.3	614	4	Q96GA6	Q96ga6 homo sapien
35	344	54.3	241	11	Q921A6	Q921a6 mus musculu
36	343.5	54.2	142	11	Q924Q1	Q924q1 mus musculu
37	339.5	53.5	119	4	Q9UL73	Q9ul73 homo sapien
38	338.5	53.4	473	11	Q9D8L4	Q9d814 mus musculu
39	335	52.8	145	11	Q924Q7	Q924q7 mus musculu
40	332	52.4	159	4	Q96QS0	Q96qs0 homo sapien
41	331.5	52.3	146	11	Q924Q8	Q924q8 mus musculu
42	331.5	52.3	481	11	Q91WT1	Q91wt1 mus musculu
43	331	52.2	109	11	Q9JL75	Q9jl75 mus musculu
44	330	52.1	121	11	Q99NG4	Q99ng4 mus musculu
45	329.5	52.0	146	11	Q924R8	Q924r8 mus musculu

ALIGNMENTS

RESULT 1
Q9UL93
ID Q9UL93 PRELIMINARY; PRT; 116 AA.
AC Q9UL93;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035021; AAD56257.1; -.
DR HSSP; P01772; 2FB4.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGv; 1.
FT NON_TER 1 1
FT NON_TER 116 116
SQ SEQUENCE 116 AA; 12434 MW; 0DA0348154DD6061 CRC64;

Query Match 86.2%; Score 546.5; DB 4; Length 116;
Best Local Similarity 90.6%; Pred. No. 9.3e-48;
Matches 106; Conservative 2; Mismatches 8; Indels 1; Gaps 1;

```
Qy       2 VQLVESGGGVVQPGRSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVTFISYDGNNKYYA 61
          ||||||||||||||||||||||||||||||||||||||||||||||||||| |||||:|||||
Db       1 VQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYYA 60
```

```
DE   Ig heavy chain V-III region GA.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=74175307; PubMed=4208843;
RA   Florent G., Lehman D., Putnam F.W.;
RT   "The switch point in mu heavy chains of human IgM immunoglobulins.";
RL   Biochemistry 13:2482-2498(1974).
CC   -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S
CC       MACROGLOBULIN.
DR   PIR; A02052; M3HUGA.
DR   HSSP; P01772; 2FB4.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW    mmunoglobulin V region.
FT    OD_RES       1      1       PYRROLIDONE CARBOXYLIC ACID.
FT   NON_TER     122    122
SQ   SEQUENCE   122 AA;  13166 MW;  74E5B6959E84100A CRC64;

  Query Match             79.0%;  Score 501;  DB 1;  Length 122;
  Best Local Similarity   73.0%;  Pred. No. 3.6e-43;
  Matches   89;  Conservative   22;  Mismatches    7;  Indels    4;  Gaps    2;

Qy       1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVTFISYDGNNKYY 60
           ||:|||:|||| |:|||||||||||||:||:| |||||||||||:|:: |||:|:::|| .
Db       1 QVZLVZSGGGAVZPGRSLRLSCAASGFSFSTYAMHWVRQAPGKGLZWLSVISYBGBBZYY 60

Qy      61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAIYYCARTG-WLGPF---DYWGQGTLVTV 116
           | |||||||||::||:|:||:|||||||:||:|||||:|   ||      ||||:||||| :
Db      61 AASVKGRFTISRBBSKBTMYLEMNSLRAENTAVYYCARSGIALGSVAGTDYWGZGTLVTI 120

Qy     117 SS 118
           ||
Db     121 SS 122


RESULT 3
HV3I_HUMAN
ID   HV3I_HUMAN     STANDARD;      PRT;   119 AA.
AC   P01770;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE    g heavy chain V-III region NIE.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=77070269; PubMed=826475;
RA   Ponstingl H., Hilschmann N.;
RT   "The rule of antibody structure. The primary structure of a
RT   monoclonal IgG1 immunoglobulin (myeloma protein Nie). III. The
RT   chymotryptic peptides of the H-chain, alignment of the tryptic
RT   peptides and discussion of the complete structure.";
RL   Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).
RN   [2]
RP   DISULFIDE BOND.
RX   MEDLINE=77070267; PubMed=1002129;
RA   Dreker L., Schwarz J., Reichel W., Hilschmann N.;
RT   "Rule of antibody structure. The primary structure of a monoclonal
RT   IgG1 immunoglobulin (myeloma protein Nie), I: Purification and
RT   characterization of the protein, the L- and H-chains, the
RT   cyanogen bromide cleavage products, and the disulfide bridges.";
RL   Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
CC   -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG1 MYELOMA
CC       PROTEIN.
DR   PIR; A02053; G1HUNI.
DR   HSSP; P01772; 2FB4.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region.
FT   MOD_RES       1      1       PYRROLIDONE CARBOXYLIC ACID.
FT   DISULFID     22     96
FT   NON_TER     119    119
SQ   SEQUENCE   119 AA;  13242 MW;  C96935A6E55E165B CRC64;

  Query Match             78.5%;  Score 497.5;  DB 1;  Length 119;
  Best Local Similarity   78.5%;  Pred. No. 7.7e-43;
  Matches   95;  Conservative   11;  Mismatches   10;  Indels    5;  Gaps    2;

Qy       1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVTFISYDGNNKYY 60
           |||||:|||||||||||||||||||||| ||:|||||||||||||  :||:|::|:|
Db       1 QVQLVQSGGGVVQPGRSLRLSCAASGFTFSRYTIHWVRQAPGKGLEWVAVMSYBGBBKHY 60

Qy      61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAIYYCAR---TGWLGPFDYWGQGTLVTVS 117
           |||| |||||||::|||||||  |||||  ||||:|||||    |      | :||||||||||
Db      61 ADSVNGRFTISRNDSKNTLYLNMNSLRPEDTAVYYCARIRDTAMF--FAHWGQGTLVTVS 118

Qy     118 S 118
           |
Db     119 S 119


RESULT 4
HV3J_HUMAN
ID   HV3J_HUMAN     STANDARD;      PRT;   121 AA.
AC   P01771;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig heavy chain V-III region HIL.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=79124695; PubMed=420800;
RA   Chiu Y.-Y.H., Lopez de Castro J.A., Poljak R.J.;
RT   "Amino acid sequence of the VH region of human myeloma
RT   cryoimmunoglobulin IgG Hil.";
RL   Biochemistry 18:553-560(1979).
CC   -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG1 MYELOMA
CC       PROTEIN.
DR   PIR; A02054; G1HUHL.
DR   HSSP; P01772; 2FB4.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region.
FT   MOD_RES       1      1       PYRROLIDONE CARBOXYLIC ACID.
FT   NON_TER     121    121
SQ   SEQUENCE   121 AA;  13566 MW;  480FC53610EF5DAB CRC64;

  Query Match             76.7%;  Score 486.5;  DB 1;  Length 121;
  Best Local Similarity   75.6%;  Pred. No. 9.8e-42;
  Matches   93;  Conservative   10;  Mismatches   13;  Indels    7;  Gaps    2;

Qy       1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVTFISYDGNNKYY 60
           ||:||::|||||||||||||| |||||||:| ||||||||||||||  | |:|:  ||
Db       1 QVKLVQAGGGVVQPGRSLRLSCIASGFTFSNYGMHWVRQAPGKGLEWVAVIWYNGSRTYY 60

Qy      61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAIYYCAR-----TGWLGPFDYWGQGTLVT 115
           |||||||||||||| |||::||||| ||||:|||||      | :   ||||||| |||
Db      61 GDSVKGRFTISRDNSKRTLYMZMNSLRTEDTAVYYCARDPDILTAF--SFDYWGQGVLVT 118
```

GenCore version 5.1.4_p5_4578

OM protein - protein search, using sw model

Run on: April 16, 2003, 16:57:42 ; Search time 23.186 Seconds
(without alignments)
211.085 Million cell updates/sec

Title: US-09-644-668A-17
Perfect score: 634
Sequence: 1 QVQLVESGGGVVQPGRSLRL.....TGWLGPFDYWGQGTLVTVSS 118

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	526	83.0	122	1	HV3G_HUMAN	P01768 homo sapien
2	501	79.0	122	1	HV3H_HUMAN	P01769 homo sapien
3	497.5	78.5	119	1	HV3I_HUMAN	P01770 homo sapien
4	486.5	76.7	121	1	HV3J_HUMAN	P01771 homo sapien
5	480	75.7	126	1	HV3K_HUMAN	P01772 homo sapien
6	461	72.7	114	1	HV3B_HUMAN	P01763 homo sapien
7	460	72.6	116	1	HV3T_HUMAN	P01781 homo sapien
8	452.5	71.4	119	1	HV3L_HUMAN	P01773 homo sapien
9	450	71.0	136	1	HV16_MOUSE	P01783 mus musculu
10	436	68.8	120	1	HV3U_HUMAN	P01782 homo sapien
11	435	68.6	117	1	HV3C_HUMAN	P01764 homo sapien
12	432	68.1	119	1	HV3M_HUMAN	P01774 homo sapien
13	431.5	68.1	120	1	HV3E_HUMAN	P01766 homo sapien
14	430	67.8	119	1	HV3N_HUMAN	P01775 homo sapien
15	424	66.9	122	1	HV3A_HUMAN	P01762 homo sapien
16	423.5	66.8	115	1	HV3D_HUMAN	P01765 homo sapien
17	421	66.4	119	1	HV38_MOUSE	P01808 mus musculu
18	419.5	66.2	115	1	HV3F_HUMAN	P01767 homo sapien
19	417.5	65.9	116	1	HV05_CARAU	P19181 carassius a
20	414	65.3	114	1	HV01_CANFA	P01784 canis famil
21	413.5	65.2	115	1	HV32_MOUSE	P01801 mus musculu
22	413	65.1	119	1	HV37_MOUSE	P01807 mus musculu
23	412.5	65.1	142	1	HV01_RAT	P01805 rattus norv
24	411	64.8	117	1	HV3O_HUMAN	P01776 homo sapien
25	408.5	64.4	113	1	HV30_MOUSE	P01799 mus musculu
26	406	64.0	119	1	HV40_MOUSE	P01810 mus musculu
27	405.5	64.0	117	1	HV02_CANFA	P01785 canis famil
28	403.5	63.6	113	1	HV27_MOUSE	P01796 mus musculu
29	402.5	63.5	118	1	HV39_MOUSE	P01809 mus musculu
30	400.5	63.2	113	1	HV31_MOUSE	P01800 mus musculu
31	399.5	63.0	115	1	HV33_MOUSE	P01802 mus musculu
32	398	62.8	117	1	HV54_MOUSE	P18525 mus musculu
33	397.5	62.7	113	1	HV28_MOUSE	P01797 mus musculu
34	397	62.6	111	1	HV35_MOUSE	P01804 mus musculu
35	396.5	62.5	113	1	HV34_MOUSE	P01803 mus musculu
36	396	62.5	122	1	HV20_MOUSE	P01789 mus musculu
37	393.5	62.1	113	1	HV29_MOUSE	P01798 mus musculu
38	393.5	62.1	116	1	HV3Q_HUMAN	P01778 homo sapien
39	393.5	62.1	117	1	HV17_MOUSE	P01786 mus musculu
40	392.5	61.9	117	1	HV41_MOUSE	P01811 mus musculu
41	392	61.8	117	1	HV55_MOUSE	P18526 mus musculu
42	390.5	61.6	123	1	HV25_MOUSE	P01794 mus musculu
43	390	61.5	118	1	HV3V_HUMAN	P80419 homo sapien
44	389.5	61.4	123	1	HV24_MOUSE	P01793 mus musculu
45	389	61.4	119	1	HV3P_HUMAN	P01777 homo sapien

ALIGNMENTS

RESULT 1
HV3G_HUMAN
ID HV3G_HUMAN STANDARD; PRT; 122 AA.
AC P01768;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V-III region CAM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=81013859; PubMed=6774332;
RA Lehman D.W., Putnam F.W.;
RT "Amino acid sequence of the variable region of a human mu chain:
RT location of a possible JH segment.";
RL Proc. Natl. Acad. Sci. U.S.A. 77:3239-3243(1980).
CC -!- MISCELLANEOUS: THIS MU CHAIN WAS ISOLATED FROM THE PLASMA OF A
CC PATIENT WITH MACROGLOBULINEMIA.
DR PIR; A02051; M3HUAM.
DR HSSP; P01772; 2FB4.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGv; 1.
KW Immunoglobulin V region.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT NON_TER 122 122
SQ SEQUENCE 122 AA; 13668 MW; A42D0F17D252F1C2 CRC64;

Query Match 83.0%; Score 526; DB 1; Length 122;
Best Local Similarity 79.5%; Pred. No. 1.2e-45;
Matches 97; Conservative 12; Mismatches 9; Indels 4; Gaps 1;

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Qy       1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVTFISYDGNNKYY 60
           ||:|||||||:|||||||||||||||||:| |||||| |||||||  |||:|::|||
Db       1 QVELVESGGGVVZPGRSLRLSCAASGFTFSNYAMHWVRQPPGKGLEWVAVISYBGBBKYY 60

Qy      61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAIYYCART----GWLGPFDYWGQGTLVTV 116
           |:|||||||||||:||:|||||||||||:||:|||||     |    |:||||||||||
Db      61 ABSVKGRFTISRDBSKBTLYLQMNSLRAEBTAVYYCARDRPLYGBYRAFNYWGQGTLVTV 120

Qy     117 SS 118
           ||
Db     121 SS 122
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RESULT 2
HV3H_HUMAN
ID HV3H_HUMAN STANDARD; PRT; 122 AA.
AC P01769;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)

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A;Cross-references: GDB:118731; OMIM:146910
A;Map position: 14q32.33-14q32.33
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

  Query Match            88.7%;  Score 562.5;  DB 2;  Length 121;
  Best Local Similarity  89.3%;  Pred. No. 2.3e-43;
  Matches  109;  Conservative    2;  Mismatches    6;  Indels    5;  Gaps    2;

Qy       1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVTFISYDGNNKYY 60
           |||||||||||||||||||||||||||||||||| ||||||||||||||  |||||:||||
Db       1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60

Qy      61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAIYYCART----GWLGPFDYWGQGTLVTV 116
           ||||||||||||||||||||||||||||||:|||||     ||   ||||||||||||
Db      61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRKDWGW-ALFDYWGQGTLVTV 119

Qy     117 SS 118
           ||
Db     120 SS 121


RESULT 3
S31598
Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S31598
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A;Description: Mechanisms that generate human immunoglobulin diversity operate from the
A;Reference number: S31585
A;Accession: S31598
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-135 <CUI>
A;Cross-references: EMBL:Z14170; NID:g31001; PIDN:CAA78539.1; PID:g31002
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;31-114/Domain: immunoglobulin homology <IMM>

  Query Match            88.4%;  Score 560.5;  DB 2;  Length 135;
  Best Local Similarity  89.1%;  Pred. No. 3.8e-43;
  Matches  106;  Conservative    4;  Mismatches    8;  Indels    1;  Gaps    1;

Qy       1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVTFISYDGNNKYY 60
           |||||||||||||||| |||||||||||||||| ||||||||||||| || |||:||||
Db      17 QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIRYDGSNKYY 76

Qy      61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAIYYCARTGW-LGPFDYWGQGTLVTVSS 118
           ||||||||||||||||||||||||||||:||||:  | :  ||||||||||||||
Db      77 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKISWEVSRFDYWGQGTLVTVSS 135


RESULT 4
S31116
Ig heavy chain - human
C;Species: Homo sapiens (man)
C;Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C;Accession: S31116
R;Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman
Eur. J. Immunol. 22, 247-251, 1992
A;Title: Restricted utilization of germ-line V(H)3 genes and short diverse third complem
A;Reference number: S31104; MUID:92111633; PMID:1730252
A;Accession: S31116
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
A;Residues: 1-118 <RAA>
A;Cross-references: EMBL:X62966
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

  Query Match            87.4%;  Score 554;  DB 2;  Length 118;
  Best Local Similarity  89.0%;  Pred. No. 1.3e-42;
  Matches  105;  Conservative    3;  Mismatches   10;  Indels    0;  Gaps    0;

Qy       1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVTFISYDGNNKYY 60
           |||||||||||||||||||||||||||||||||| ||||||||||||||  |||||:||||
Db       1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNKYY 60

Qy      61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAIYYCARTGWLGPFDYWGQGTLVTVSS 118
           |||||||||||||||||||||||||||||||:||||  |    || |||||:|||||
Db      61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCATDGGKAAFDIWGQGTMVTVSS 118


RESULT 5
S31701
Ig heavy chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S31701
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A;Description: Mechanisms that generate human immunoglobulin diversity operate from the
A;Reference number: S31585
A;Accession: S31701
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-137 <CUI>
A;Cross-references: EMBL:Z14177; NID:g31020; PIDN:CAA78546.1; PID:g31021
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMM>

  Query Match            87.2%;  Score 553;  DB 2;  Length 137;
  Best Local Similarity  87.3%;  Pred. No. 1.8e-42;
  Matches  103;  Conservative    4;  Mismatches   11;  Indels    0;  Gaps    0;

Qy       1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVTFISYDGNNKYY 60
           |||||||||||||||||||||||||||||||||| ||||||||||||||  |||||:||||
Db      20 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 79

Qy      61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAIYYCARTGWLGPFDYWGQGTLVTVSS 118
           |||||||||:|||||||||||||||||||:||||  |   || |||||:|||||
Db      80 PDSVKGRFTITRDNSKNTLYLQMNSLRAEDTAVYYCATPNWNDAFDIWGQGTMVTVSS 137


RESULT 6
S31117
Ig heavy chain - human
C;Species: Homo sapiens (man)
C;Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C;Accession: S31117
R;Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman
Eur. J. Immunol. 22, 247-251, 1992
A;Title: Restricted utilization of germ-line V(H)3 genes and short diverse third complem
A;Reference number: S31104; MUID:92111633; PMID:1730252
A;Accession: S31117
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
A;Residues: 1-122 <RAA>
A;Cross-references: EMBL:X62967
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

  Query Match            87.1%;  Score 552;  DB 2;  Length 122;
  Best Local Similarity  87.7%;  Pred. No. 2e-42;
  Matches  107;  Conservative    3;  Mismatches    8;  Indels    4;  Gaps    1;

Qy       1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVTFISYDGNNKYY 60
           |||||||||||||||||||||||||||||||||| ||||||||||||||  | |||:||||
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GenCore version 5.1.4_p5_4578

OM protein - protein search, using sw model

Run on: April 16, 2003, 17:11:36 ; Search time 36.4351 Seconds
(without alignments)
311.344 Million cell updates/sec

Title: US-09-644-668A-17
Perfect score: 634
Sequence: 1 QVQLVESGGGVVQPGRSLRL.....TGWLGPFDYWGQGTLVTVSS 118

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	566.5	89.4	121	2	S19666	Ig heavy chain V r
2	562.5	88.7	121	2	G36005	Ig heavy chain V r
3	560.5	88.4	135	2	S31598	Ig heavy chain V r
4	554	87.4	118	2	S31116	Ig heavy chain - h
5	553	87.2	137	2	S31701	Ig heavy chain V r
6	552	87.1	122	2	S31117	Ig heavy chain - h
7	551	86.9	140	2	S70442	Ig heavy chain pre
8	548.5	86.5	134	2	S31679	Ig heavy chain V r
9	548	86.4	114	2	S46390	Ig heavy chain V r
10	547	86.3	122	2	E36005	Ig heavy chain V r
11	545	86.0	120	2	S31112	Ig heavy chain - h
12	544.5	85.9	132	2	S31603	Ig heavy chain V r
13	543.5	85.7	119	2	F36005	Ig heavy chain V r
14	541.5	85.4	133	2	A49028	Ig heavy chain V-I
15	541	85.3	139	2	S31674	Ig heavy chain V r
16	540.5	85.3	130	2	S31601	Ig heavy chain V r
17	527	83.1	114	2	S46392	Ig heavy chain V r
18	526.5	83.0	130	2	PL0098	Ig heavy chain pre
19	526	83.0	122	1	M3HUAM	Ig heavy chain V-I
20	525	82.8	128	2	S48797	Ig heavy chain V r
21	524.5	82.7	109	2	PH1646	Ig heavy chain V r
22	524	82.6	133	2	S31510	Ig heavy chain - h
23	522	82.3	151	2	A60943	Ig heavy chain pre
24	520.5	82.1	123	2	S38493	Ig heavy chain - h
25	517	81.5	114	2	S46391	Ig heavy chain V r
26	516.5	81.5	119	2	C36005	Ig heavy chain V r
27	515.5	81.3	109	2	PH1644	Ig heavy chain V r
28	510	80.4	120	2	S44111	Ig heavy chain V-D
29	509.5	80.4	111	2	PH1645	Ig heavy chain V r
30	509	80.3	122	2	S69910	Ig V-D-J region (K
31	508.5	80.2	111	2	PH1643	Ig heavy chain V r
32	508.5	80.2	119	2	S31108	Ig heavy chain - h
33	507.5	80.0	143	2	S23624	Ig heavy chain V r
34	506.5	79.9	123	2	S31114	Ig heavy chain - h
35	506	79.8	120	2	S48798	Ig heavy chain V r
36	505	79.7	118	2	S31677	Ig heavy chain V r
37	504.5	79.6	117	2	S78486	Ig heavy chain V r
38	503.5	79.4	140	2	S31686	Ig heavy chain V r
39	502.5	79.3	119	2	S31107	Ig heavy chain - h
40	501	79.0	122	1	M3HUGA	Ig heavy chain V-I
41	501	79.0	136	2	S31587	Ig heavy chain V r
42	499	78.7	108	2	PH1642	Ig heavy chain V r
43	498.5	78.6	113	2	S38490	Ig heavy chain - h
44	498.5	78.6	119	2	D36005	Ig heavy chain V r
45	498	78.5	124	2	S20782	Ig heavy chain V r

ALIGNMENTS

RESULT 1
S19666
Ig heavy chain V region (VH3DJH4) - human
C;Species: Homo sapiens (man)
C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 20-Jun-2000
C;Accession: S19666
R;Marks, J.D.; Hoogenboom, H.R.; Bonnert, T.P.; McCafferty, J.; Griffiths, A.D.; Wint
J. Mol. Biol. 222, 581-597, 1991
A;Title: By-passing immunization. Human antibodies from V-gene libraries displayed on
A;Reference number: S19663; MUID:92085276; PMID:1748994
A;Accession: S19666
A;Molecule type: mRNA
A;Residues: 1-121 <MAR>
A;Cross-references: EMBL:X61646; NID:g37688; PIDN:CAA43827.1; PID:g1335369
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 89.4%; Score 566.5; DB 2; Length 121;
Best Local Similarity 89.3%; Pred. No. 9.9e-44;
Matches 108; Conservative 5; Mismatches 5; Indels 3; Gaps 1;

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Qy       1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVTFISYDGNNKYY 60
           |||||:|||||||||||||||||||||||||| |||||||||||||||  |||||:||||
Db       1 QVQLVQSGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNKYY 60

Qy      61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAIYYCARTGW---LGPFDYWGQGTLVTVS 117
           ||||||||||||||||||||||||||||||||:||||:||:    | ||||||||||||||
Db      61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKTGYSSGWGYFDYWGQGTLVTVS 120

Qy     118 S 118
           |
Db     121 S 121
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RESULT 2
G36005
Ig heavy chain V region (M74) - human
C;Species: Homo sapiens (man)
C;Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 16-Dec-1998
C;Accession: G36005
R;Schroeder Jr., H.W.; Wang, J.Y.
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
A;Title: Preferential utilization of conserved immunoglobulin heavy chain variable ge
A;Reference number: A36005; MUID:90349571; PMID:2117273
A;Accession: G36005
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-121 <SCH>
A;Cross-references: GB:M34031
C;Genetics:
A;Gene: GDB:IGH@; IGHDY1

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Qy       1 EIVLTQSPGTLSLSPGERATLSCRASQSVGSSYLAWYQQKPGQAPRLLIYGAFSRATGIP 60
           |||||||||||||||||||||||||||| |||||||||||||||||||| |||||||
Db       1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60

Qy      61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPWTFGQGTKVEIK 108
           ||||||||||||||||||||||||||||||:||:||||||||||
Db      61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGNSPYTFGQGTKVEIK 108


RESULT 2
US-09-240-274-178
; Sequence 178, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
;  APPLICANT: Siegel, Donald L.
;  TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
;  TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
;  FILE REFERENCE: 09596-42U2
;     ENT APPLICATION NUMBER: US/09/240,274
;     ENT FILING DATE: 1999-01-29
;  EARLIER APPLICATION NUMBER: 60/081,380
;  EARLIER FILING DATE: 1998-04-10
;  EARLIER APPLICATION NUMBER: 60/028,550
;  EARLIER FILING DATE: 1996-10-11
;  NUMBER OF SEQ ID NOS: 224
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 178
;   LENGTH: 108
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: anti-Rh(D) antibody clone SH52
US-09-240-274-178

  Query Match             95.1%;  Score 538;  DB 4;  Length 108;
  Best Local Similarity   97.1%;  Pred. No. 1.8e-42;
  Matches  102;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4 LTQSPGTLSLSPGERATLSCRASQSVGSSYLAWYQQKPGQAPRLLIYGAFSRATGIPDRF 63
           |||||||||||||||||||||||: |||||||||||||||||||| |||||||||
Db       3 LTQSPGTLSLSPGERATLSCRASQSISSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRF 62

Qy      64 SGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPWTFGQGTKVEIK 108
           |||||||||||||||||||||||||||||||||||||||||||||
Db      63 SGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPWTFGQGTKVEIK 107


RESULT 3
US-08-232-081B-42
; Sequence 42, Application US/08232081B
; Patent No. 5886152
;  GENERAL INFORMATION:
;    APPLICANT:  NAKATANI, TOMOYUKI
;    APPLICANT:  GOMI, HIDEYUKI
;    APPLICANT:  WIJDENES, JOHN
;    APPLICANT:  NOGUCHI, HIROSHI
;    TITLE OF INVENTION:  HUMANIZED B-B10
;    NUMBER OF SEQUENCES:  42
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BIRCH, STEWART, KOLASCH AND BIRCH
;      STREET:  PO BOX 747
;      CITY:  FALLS CHURCH
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22040-0747
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/232,081B
;      FILING DATE:
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SVENSSON, LEONARD R
;      REGISTRATION NUMBER:  30,330
;      REFERENCE/DOCKET NUMBER:  20-3484
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703) 205-8000
;      TELEFAX:  (703) 205-8050
;  INFORMATION FOR SEQ ID NO:  42:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  108 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-232-081B-42

  Query Match             94.7%;  Score 536;  DB 2;  Length 108;
  Best Local Similarity   96.3%;  Pred. No. 2.7e-42;
  Matches  104;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 EIVLTQSPGTLSLSPGERATLSCRASQSVGSSYLAWYQQKPGQAPRLLIYGAFSRATGIP 60
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Qy      61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPWTFGQGTKVEIK 108
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Db      61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPLTFGQGTKVEIK 108


RESULT 4
US-08-488-113B-150
; Sequence 150, Application US/08488113B
; Patent No. 5744580
;  GENERAL INFORMATION:
;    APPLICANT:  Better, Marc D.
;    APPLICANT:  Carroll, Stephen F.
;    APPLICANT:  Studnika, Gary M.
;    TITLE OF INVENTION:  Immunotoxins Comprising Ribosome-Inactivating
;    TITLE OF INVENTION:  Proteins
;    NUMBER OF SEQUENCES:  169
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  McAndrews, Held & Malloy, Ltd.
;      STREET:  500 West Madison Street, 34th floor
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60661
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/488,113B
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/425,336
;      FILING DATE:  18-APR-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/064,691
;      FILING DATE:  12-MAY-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/988,430
;      FILING DATE:  09-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/901,707
;      FILING DATE:  19-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/787,567
;      FILING DATE:  04-NOV-1991
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GenCore version 5.1.4_p5_4578

OM protein - protein search, using sw model

Run on: April 16, 2003, 17:15:40 ; Search time 27.6632 Seconds
(without alignments)
114.870 Million cell updates/sec

Title: US-09-644-668A-7
Perfect score: 566
Sequence: 1 EIVLTQSPGTLSLSPGERAT.....CQQYGSSPWTFGQGTKVEIK 108

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	540	95.4	109	4	US-09-025-769B-16	Sequence 16, Appl
2	538	95.1	108	4	US-09-240-274-178	Sequence 178, App
3	536	94.7	108	2	US-08-232-081B-42	Sequence 42, Appl
4	532	94.0	108	1	US-08-488-113B-150	Sequence 150, App
5	532	94.0	108	1	US-08-477-484B-150	Sequence 150, App
6	532	94.0	108	2	US-08-646-360-150	Sequence 150, App
7	532	94.0	108	4	US-08-839-765-150	Sequence 150, App
8	532	94.0	108	4	US-09-136-389-150	Sequence 150, App
9	532	94.0	108	4	US-09-610-838-150	Sequence 150, App
10	515.5	91.1	107	1	US-08-107-669D-14	Sequence 14, Appl
11	515.5	91.1	107	1	US-08-472-788A-14	Sequence 14, Appl
12	515.5	91.1	107	2	US-08-477-531B-14	Sequence 14, Appl
13	515.5	91.1	107	2	US-08-082-842A-14	Sequence 14, Appl
14	515	91.0	108	1	US-07-634-278-86	Sequence 86, Appl
15	515	91.0	108	1	US-08-477-728-86	Sequence 86, Appl
16	515	91.0	108	1	US-08-474-040-86	Sequence 86, Appl
17	515	91.0	108	1	US-08-487-200-86	Sequence 86, Appl
18	515	91.0	108	4	US-08-484-537-86	Sequence 86, Appl
19	513	90.6	108	1	US-08-276-852-86	Sequence 86, Appl
20	513	90.6	108	1	US-08-899-575-86	Sequence 86, Appl
21	513	90.6	108	1	US-08-899-575-86	Sequence 86, Appl
22	513	90.6	108	5	PCT-US95-08743-86	Sequence 86, Appl
23	511	90.3	150	4	US-08-862-124-5	Sequence 5, Appli
24	511	90.3	287	4	US-08-862-124-17	Sequence 17, Appl
25	511	90.3	304	4	US-08-862-124-14	Sequence 14, Appl
26	510.5	90.2	107	2	US-08-652-558-49	Sequence 49, Appl
27	502	88.7	108	1	US-08-276-852-99	Sequence 99, Appl
28	502	88.7	108	1	US-08-899-575-99	Sequence 99, Appl
29	502	88.7	108	1	US-08-899-575-99	Sequence 99, Appl
30	502	88.7	108	5	PCT-US95-08743-99	Sequence 99, Appl
31	501	88.5	129	2	US-08-480-774A-4	Sequence 4, Appli
32	493	87.1	110	4	US-09-025-769B-30	Sequence 30, Appl
33	493	87.1	110	4	US-09-025-769B-47	Sequence 47, Appl
34	492.5	87.0	134	1	US-08-405-034-4	Sequence 4, Appli
35	491	86.7	109	1	US-08-162-102C-23	Sequence 23, Appl
36	491	86.7	109	5	PCT-US93-08786-23	Sequence 23, Appl
37	489.5	86.5	109	1	US-08-276-852-147	Sequence 147, App
38	489.5	86.5	109	1	US-08-899-575-147	Sequence 147, App
39	489.5	86.5	109	1	US-08-899-575-147	Sequence 147, App
40	489.5	86.5	109	5	PCT-US95-08743-147	Sequence 147, App
41	487	86.0	104	1	US-08-276-852-100	Sequence 100, App
42	487	86.0	104	1	US-08-899-575-100	Sequence 100, App
43	487	86.0	104	1	US-08-899-575-100	Sequence 100, App
44	487	86.0	104	5	PCT-US95-08743-100	Sequence 100, App
45	487	86.0	107	1	US-08-276-852-90	Sequence 90, Appl

ALIGNMENTS

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RESULT 1
US-09-025-769B-16
; Sequence 16, Application US/09025769B
; Patent No. 6300064
; GENERAL INFORMATION:
;   APPLICANT:  Knappik, Achim
;   APPLICANT:  Pack, Peter
;   APPLICANT:  Ilag, Vic
;   APPLICANT:  Ge, Liming
;   APPLICANT:  Moroney, Simon
;   APPLICANT:  Plueckthun, Andreas
;   TITLE OF INVENTION:  Protein/(Poly)peptide libraries
;   NUMBER OF SEQUENCES:  373
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  James F. Haley, Jr., Esq. c/o Fish & Neave
;     STREET:  1251 Avenue of the Americas
;     CITY:  New York
;     STATE:  New York
;     COUNTRY:  USA
;     ZIP:  10021
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Floppy disk
;     COMPUTER:  IBM PC compatible
;     OPERATING SYSTEM:  PC-DOS/MS-DOS
;     SOFTWARE:  PatentIn Release #1.0, Version #1.30 (EPO)
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/09/025,769B
;     FILING DATE:  18-FEB-1998
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  EP 95 11 3021.0
;     FILING DATE:  18-AUG-1995
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  James F. Haley, Jr., Esq.
;     REGISTRATION NUMBER:  27,794
;     REFERENCE/DOCKET NUMBER:  MORPHO/5
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  (212)596-9000
;     TELEFAX:  (212)596-9090
; INFORMATION FOR SEQ ID NO:  16:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH:  109 amino acids
;     TYPE:  amino acid
;     STRANDEDNESS:
;     TOPOLOGY:  linear
;   MOLECULE TYPE:  protein
US-09-025-769B-16

  Query Match           95.4%;  Score 540;  DB 4;  Length 109;
  Best Local Similarity  96.3%;  Pred. No. 1.2e-42;
  Matches  104;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;
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; GENERAL INFORMATION:
;  APPLICANT: Ruben et al.
;  TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
;  FILE REFERENCE: PF523
;  CURRENT APPLICATION NUMBER: US/09/880,748
;  CURRENT FILING DATE:  2001-06-15
;  PRIOR APPLICATION NUMBER: 60/212,210
;  PRIOR FILING DATE: 2000-06-15
;  PRIOR APPLICATION NUMBER: 60/240,816
;  PRIOR FILING DATE: 2000-10-17
;  PRIOR APPLICATION NUMBER: 60/276,248
;  PRIOR FILING DATE: 2001-03-16
;  PRIOR APPLICATION NUMBER: 60/277,379
;  PRIOR FILING DATE: 2001-03-21
;  PRIOR APPLICATION NUMBER: 60/293,499
;  PRIOR FILING DATE: 2001-05-25
;  NUMBER OF SEQ ID NOS: 3239
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1499
;     GTH: 253
;     PE: PRT
;   ORGANISM: Homo sapiens
US-09-880-748-1499

  Query Match             91.3%;  Score 517;  DB 9;  Length 253;
  Best Local Similarity   93.5%;  Pred. No. 8.4e-30;
  Matches  101;  Conservative    1;  Mismatches    6;  Indels    0;  Gaps    0;

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Db     145 ETTLTQSPGTLSLSPGERATLSCRASQSVRNSYLAWYQQKPGQAPRLLIYGASSRATGIP 204

Qy      61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPWTFGQGTKVEIK 108
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Db     205 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPVTFGGGTKVEIK 252


RESULT 3
US-09-880-748-1264
; Sequence 1264, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
;  APPLICANT: Ruben et al.
;  TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
;  FILE REFERENCE: PF523
;  CURRENT APPLICATION NUMBER: US/09/880,748
;  CURRENT FILING DATE:  2001-06-15
;     OR APPLICATION NUMBER: 60/212,210
;     OR FILING DATE: 2000-06-15
;  PRIOR APPLICATION NUMBER: 60/240,816
;  PRIOR FILING DATE: 2000-10-17
;  PRIOR APPLICATION NUMBER: 60/276,248
;  PRIOR FILING DATE: 2001-03-16
;  PRIOR APPLICATION NUMBER: 60/277,379
;  PRIOR FILING DATE: 2001-03-21
;  PRIOR APPLICATION NUMBER: 60/293,499
;  PRIOR FILING DATE: 2001-05-25
;  NUMBER OF SEQ ID NOS: 3239
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1264
;   LENGTH: 246
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-880-748-1264

  Query Match             90.9%;  Score 514.5;  DB 9;  Length 246;
  Best Local Similarity   95.4%;  Pred. No. 1.2e-29;
  Matches  103;  Conservative    0;  Mismatches    4;  Indels    1;  Gaps    1;

Qy       1 EIVLTQSPGTLSLSPGERATLSCRASQSVGSSYLAWYQQKPGQAPRLLIYGAFSRATGIP 60
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Db     139 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 198

Qy      61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPWTFGQGTKVEIK 108
           |||||||||||||||||||||||||||||||||| ||| |||||||
Db     199 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSS-LTFGGGTKVEIK 245


RESULT 4
US-08-844-215-8
; Sequence 8, Application US/08844215
; Patent No. US20020016445A1
;  GENERAL INFORMATION:
;    APPLICANT:  PERSSON, MATS AXEL
;    APPLICANT:  ALLANDER, TOBIAS ERIK
;    TITLE OF INVENTION:  HUMAN MONOCLONAL ANTIBODIES SPECIFIC FOR
;    TITLE OF INVENTION:  HEPATITIS C VIRUS (HCV) E2 ANTIGEN
;    NUMBER OF SEQUENCES:  34
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  ROBINS & ASSOCIATES
;      STREET:  90 MIDDLEFIELD ROAD, SUITE 200
;      CITY:  MENLO PARK
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94025
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/844,215
;      FILING DATE:  17-APR-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/635,109
;      FILING DATE:  19-APR-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MCCRACKEN, THOMAS P.
;      REGISTRATION NUMBER:  38,548
;      REFERENCE/DOCKET NUMBER:  80146.002
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650) 325-7812
;      TELEFAX:  (650) 325-7823
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  107 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-844-215-8

  Query Match             90.8%;  Score 514;  DB 8;  Length 107;
  Best Local Similarity   93.3%;  Pred. No. 6.8e-30;
  Matches   98;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       4 LTQSPGTLSLSPGERATLSCRASQSVGSSYLAWYQQKPGQAPRLLIYGAFSRATGIPDRF 63
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Db       3 LTQSPGTLSLSPGERATLSCRASQSVSSNYLAWYQQRPGQAPRLLIYGASSRATGIPDRF 62

Qy      64 SGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPWTFGQGTKVEIK 108
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Db      63 SGSGSGTDFTLTISRLEPEDFAVYYCQLYGNSRWTFGQGTKVEIK 107


RESULT 5
US-09-782-397-5
; Sequence 5, Application US/09782397
; Publication No. US20030021779A1
;  GENERAL INFORMATION:
;       APPLICANT: Dan, Michael D.
;                  Maiti, Pradip K.
;                  Kaplan, Howard A.
;       TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS H11, THAT
;                           SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODIN
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OM protein - protein search, using sw model

Run on: April 16, 2003, 17:21:54 ; Search time 31.8316 Seconds
(without alignments)
256.547 Million cell updates/sec

Title: US-09-644-668A-7
Perfect score: 566
Sequence: 1 EIVLTQSPGTLSLSPGERAT.....CQQYGSSPWTFGQGTKVEIK 108

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 288829 seqs, 75613885 residues

Total number of hits satisfying chosen parameters: 288829

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
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2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
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4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
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12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
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14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	538	95.1	108	9	US-09-848-798-178	Sequence 178, App
2	517	91.3	253	9	US-09-880-748-1499	Sequence 1499, Ap
3	514.5	90.9	246	9	US-09-880-748-1264	Sequence 1264, Ap
4	514	90.8	107	8	US-08-844-215-8	Sequence 8, Appli
5	511	90.3	150	9	US-09-782-397-5	Sequence 5, Appli
6	511	90.3	287	9	US-09-782-397-17	Sequence 17, Appl
7	511	90.3	304	9	US-09-782-397-14	Sequence 14, Appl
8	508	89.8	108	9	US-09-300-425B-21	Sequence 21, Appl
9	507	89.6	105	10	US-09-828-708-3	Sequence 3, Appli
10	506.5	89.5	251	9	US-09-880-748-1219	Sequence 1219, Ap
11	506	89.4	107	8	US-08-844-215-10	Sequence 10, Appl
12	505.5	89.3	236	10	US-09-859-053-34	Sequence 34, Appl
13	503	88.9	105	10	US-09-828-708-7	Sequence 7, Appli
14	503	88.9	110	9	US-10-001-934-40	Sequence 40, Appl
15	500.5	88.4	212	9	US-10-006-593-118	Sequence 118, App
16	497.5	87.9	236	10	US-09-859-053-38	Sequence 38, Appl
17	493.5	87.2	252	9	US-09-880-748-1534	Sequence 1534, Ap
18	493	87.1	109	9	US-10-125-687-10	Sequence 10, Appl
19	493	87.1	109	12	US-10-025-687-10	Sequence 10, Appl
20	493	87.1	249	9	US-09-880-748-1035	Sequence 1035, Ap
21	487.5	86.1	245	9	US-09-880-748-1896	Sequence 1896, Ap
22	485.5	85.8	106	8	US-08-844-215-14	Sequence 14, Appl
23	485	85.7	96	9	US-10-194-975-82	Sequence 82, Appl
24	485	85.7	107	8	US-08-844-215-12	Sequence 12, Appl
25	484.5	85.6	254	9	US-09-880-748-905	Sequence 905, App
26	479	84.6	251	9	US-09-880-748-22	Sequence 22, Appl
27	479	84.6	251	9	US-09-880-748-24	Sequence 24, Appl
28	479	84.6	251	9	US-09-880-748-26	Sequence 26, Appl
29	479	84.6	251	9	US-09-880-748-28	Sequence 28, Appl
30	479	84.6	251	9	US-09-880-748-30	Sequence 30, Appl
31	477.5	84.4	104	10	US-09-828-708-6	Sequence 6, Appli
32	475	83.9	251	9	US-09-880-748-10	Sequence 10, Appl
33	475	83.9	251	9	US-09-880-748-12	Sequence 12, Appl
34	475	83.9	251	9	US-09-880-748-17	Sequence 17, Appl
35	475	83.9	251	9	US-09-880-748-19	Sequence 19, Appl
36	475	83.9	251	9	US-09-880-748-21	Sequence 21, Appl
37	475	83.9	251	9	US-09-880-748-23	Sequence 23, Appl
38	475	83.9	251	9	US-09-880-748-25	Sequence 25, Appl
39	475	83.9	251	9	US-09-880-748-27	Sequence 27, Appl
40	475	83.9	251	9	US-09-880-748-29	Sequence 29, Appl
41	475	83.9	251	9	US-09-880-748-31	Sequence 31, Appl
42	475	83.9	251	9	US-09-880-748-33	Sequence 33, Appl
43	475	83.9	251	9	US-09-880-748-43	Sequence 43, Appl
44	475	83.9	251	9	US-09-880-748-85	Sequence 85, Appl
45	475	83.9	251	9	US-09-880-748-178	Sequence 178, App

ALIGNMENTS

RESULT 1
US-09-848-798-178
; Sequence 178, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/848,798
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 178
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH52
US-09-848-798-178

Query Match 95.1%; Score 538; DB 9; Length 108;
Best Local Similarity 97.1%; Pred. No. 1.4e-31;
Matches 102; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```
Qy       4 LTQSPGTLSLSPGERATLSCRASQSVGSSYLAWYQQKPGQAPRLLIYGAFSRATGIPDRF 63
           |||||||||||||||||||||||: |||||||||||||||||||| ||||||||||
Db       3 LTQSPGTLSLSPGERATLSCRASQSISSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRF 62

Qy      64 SGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPWTFGQGTKVEIK 108
           ||||||||||||||||||||||||||||||||||||||||||||||
Db      63 SGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPWTFGQGTKVEIK 107
```

RESULT 2
US-09-880-748-1499
; Sequence 1499, Application US/09880748
; Publication No. US20030059937A1

XX
KW Human immunodeficiency virus-1; HIV-1; human monoclonal antibody;
KW envelope glycoprotein; gp120; diagnosis.
XX
OS Homo sapiens.
XX
PN WO200100678-A1.
XX
PD 04-JAN-2001.
XX
PF 23-JUN-2000; 2000WO-US17327.
XX
PR 30-JUN-1999; 99US-0141701.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Watkins BA, Reitz MS;
XX
DR WPI; 2001-112438/12.
DR PSDB; AAF29071.
XX
PT Novel human monoclonal antibody immunoreactive with human
PT immunodeficiency virus-1 glycoprotein gp120, useful for detecting HIV-1
PT in biological sample and providing passive immunotherapy to HIV-1
PT infected mammal -
XX
PS Claim 1; Page 66; 81pp; English.
XX
CC The present invention provides the protein and coding sequences for the
CC variable regions of human monoclonal antibodies which are immunoreactive
CC with human immunodeficiency virus-1 (HIV-1) envelope glycoprotein gp120.
CC These can be used in diagnosis and therapy of HIV-1 infection.
XX
SQ Sequence 108 AA;

Query Match 95.2%; Score 539; DB 22; Length 108;
Best Local Similarity 96.3%; Pred. No. 1.7e-33;
Matches 103; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 IVLTQSPGTLSLSPGERATLSCRASQSVGSSYLAWYQQKPGQAPRLLIYGAFSRATGIPD 61
:|||||||||||||||||||||||||| | |||||||||||||||||| ||||||||
Db 1 LVLTQSPGTLSLSPGERATLSCRASQSVSSIYLAWYQQKPGQAPRLLIYGASSRATGIPD 60

Qy 62 RFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPWTFGQGTKVEIK 108
|||||||||||||||||||||||||||||||||||||||||||||||||||
Db 61 RFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPWTFGQGTKVEIK 107

RE 6
AAM24101
ID AAM24101 standard; Protein; 384 AA.
XX
AC AAM24101;
XX
DT 12-OCT-2001 (first entry)
XX
DE Human EST encoded protein SEQ ID NO: 1626.
XX
KW Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;
KW tomato; monkey; dog; sea urchin; expressed sequence tag; EST;
KW diagnostics; forensic test; gene mapping; genetic disorder;
KW biodiversity; gene therapy; nutrition.
XX
OS Homo sapiens.
XX
PN WO200154477-A2.
XX
PD 02-AUG-2001.
XX
PF 25-JAN-2001; 2001WO-US02687.
XX
PR 25-JAN-2000; 2000US-0491404.
PR 17-JUL-2000; 2000US-0617746.
PR 03-AUG-2000; 2000US-0631451.
PR 15-SEP-2000; 2000US-0663870.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;
PI Cao Y, Drmanac RA, Zhang J, Werhman T;
XX
DR WPI; 2001-476164/51.
DR N-PSDB; AAH98760.
XX
PT Isolated polypeptide for treatment of diseases, diagnostics, raising
PT antibodies and research use -
XX
PS Claim 20; Page 1102-1103; 1275pp; English.
XX
CC The present invention provides the protein and coding sequences of novel
CC proteins from a variety of organisms, including human, dog, cat, horse,
CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
CC urchin and tomato. These were derived from expressed sequence tags (ESTs)
CC from the organism of interest. They can be used in diagnostics,
CC forensics, gene mapping, identification of mutations, to assess
CC biodiversity and for nutritional purposes. The present sequence is a
CC protein of the invention.
XX
SQ Sequence 384 AA;

Query Match 95.2%; Score 539; DB 22; Length 384;
Best Local Similarity 97.2%; Pred. No. 5.1e-33;
Matches 105; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 EIVLTQSPGTLSLSPGERATLSCRASQSVGSSYLAWYQQKPGQAPRLLIYGAFSRATGIP 60
||||||||||||||||||||||||||||| |||||||||||||||||||| |||||||
Db 167 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 226

Qy 61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPWTFGQGTKVEIK 108
|||||||||||||||||||||||||||||||||||| ||||||||||
Db 227 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPTTFGQGTKVEIK 274

RESULT 7
AAG93666
ID AAG93666 standard; Protein; 108 AA.
XX
AC AAG93666;
XX
DT 14-SEP-2001 (first entry)
XX
DE Human anti-Rh(D) antibody clone SH52 protein sequence.
XX
KW Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;
KW red blood cell; Rh phenotype; diagnosis; therapeutic.
XX
OS Homo sapiens.
XX
PN US6255455-B1.
XX
PD 03-JUL-2001.
XX
PF 29-JAN-1999; 99US-0240274.
XX
PR 11-OCT-1996; 96US-0028550.
PR 10-APR-1998; 98US-0081380.
PR 27-JUN-1997; 97US-0884045.
XX
PA (UYPE-) UNIV PENNSYLVANIA.
XX
PI Siegel DL;
XX
DR WPI; 2001-388931/41.
DR N-PSDB; AAH68723.
XX
PT New isolated protein, preferably a human anti-Rh(D) antibody for use in

GenCore version 5.1.4_p5_4578

OM protein - protein search, using sw model

Run on: April 16, 2003, 16:56:17 ; Search time 85.6421 Seconds
(without alignments)
168.037 Million cell updates/sec

Title: US-09-644-668A-7
Perfect score: 566
Sequence: 1 EIVLTQSPGTLSLSPGERAT.....CQQYGSSPWTFGQGTKVEIK 108

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_101002:*
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2: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
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4: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:*
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13: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1992.DAT:*
14: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1993.DAT:*
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20: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1999.DAT:*
21: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA2000.DAT:*
22: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:*
23: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	541.5	95.7	109	23	ABB07233	Anti-IL-4 and IL-1
2	541	95.6	235	21	AAY93702	The kappa chain of
3	541	95.6	235	21	AAY93729	The kappa chain of
4	540	95.4	129	14	AAR38672	vk325-Jk2. Homo s
5	539	95.2	108	22	AAB62770	Human HIV-1 monocl
6	539	95.2	384	22	AAM24101	Human EST encoded
7	538	95.1	108	22	AAG93666	Human anti-Rh(D) a
8	537.5	95.0	109	23	ABB07231	Anti-IL-4 receptor
9	536	94.7	384	22	AAU14461	Human novel protei
10	536	94.7	384	22	AAU14462	Human novel protei
11	536	94.7	384	22	AAU14463	Human novel protei
12	536	94.7	384	22	AAU14464	Human novel protei
13	532	94.0	109	22	AAB62773	Human HIV-1 monocl
14	529.5	93.6	226	22	AAB99374	Human interleukin
15	529.5	93.6	226	22	AAB99397	Human interleukin
16	529.5	93.6	226	22	AAB75007	Anti-IL8 monoclona
17	529.5	93.6	226	22	AAB75030	Anti-IL8 monoclona
18	528.5	93.4	109	20	AAW84096	Human V kappa subg
19	527.5	93.2	107	23	ABB07229	Anti-IL-4 receptor
20	523	92.4	108	23	AAO21549	Antibody screening
21	522.5	92.3	226	22	AAB99394	Human interleukin
22	522.5	92.3	226	22	AAB75027	Anti-IL8 monoclona
23	520.5	92.0	226	22	AAB99378	Human interleukin
24	520.5	92.0	226	22	AAB75011	Anti-IL8 monoclona
25	517.5	91.4	226	22	AAB99391	Human interleukin
26	517.5	91.4	226	22	AAB75024	Anti-IL8 monoclona
27	517	91.3	253	23	ABP45488	Human BLyS binding
28	517	91.3	307	22	AAU14225	Human novel protei
29	517	91.3	312	22	AAU14227	Human novel protei
30	516.5	91.3	226	22	AAB99390	Human interleukin
31	516.5	91.3	226	22	AAB75023	Anti-IL8 monoclona
32	515.5	91.1	107	14	AAR38593	Human lambda light
33	515.5	91.1	107	19	AAW58493	Human kappa light
34	515	91.0	108	22	AAB69689	Humanised CMV5 ant
35	515	91.0	108	23	ABG30492	Human anti-CD40 mo
36	515	91.0	108	23	ABG30495	Human anti-CD40 mo
37	514.5	90.9	226	22	AAB99376	Human interleukin
38	514.5	90.9	226	22	AAB75009	Anti-IL8 monoclona
39	514.5	90.9	246	23	ABP45253	Human BLyS binding
40	514	90.8	106	18	AAW31722	Alpha light chain
41	514	90.8	109	22	AAB62768	Human HIV-1 monocl
42	513	90.6	108	15	AAR54307	Anti-HIV gp120 imm
43	513	90.6	108	17	AAW01265	VL region of HIV n
44	513	90.6	108	21	AAY95117	Anti-gp120 antibod
45	513	90.6	108	21	AAY98226	Anti-gp120 antibod

ALIGNMENTS

RESULT 1
ABB07233
ID ABB07233 standard; Protein; 109 AA.
XX
AC ABB07233;
XX
DT 26-MAR-2002 (first entry)
XX
DE Anti-IL-4 and IL-13 receptors MAb 27A1 light chain variable region.
XX
KW Human; antibody; interleukin; IL-4; antagonist; receptor; IL-4 receptor;
KW antiarthritic; dermatological; antiulcer; antiinflammatory; cytostatic;
KW antisickling; immunosuppressive; tuberculostatic; ophthalmological;
KW IL-13; antianemic; antithyroid.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Region 24..35
FT /note= "complementarity determining region (CDR) 1"
FT Region 51..57
FT /note= "complementarity determining region (CDR) 2"
FT Region 90..99
FT /note= "complementarity determining region (CDR) 3"
XX
PN WO200192340-A2.
XX
PD 06-DEC-2001.
XX
PF 25-MAY-2001; 2001WO-US17094.
XX
PR 26-MAY-2000; 2000US-0579808.
PR 19-SEP-2000; 2000US-0665343.

```
Qy      61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPWTFGQGTKVEIK 108
           ||||||||||||||||||||||| |||||||||||| ||| |||||||
Db      61 DRFSGSGSGTDFTLTISRLEPEDCAVYYCQQYGSSPLTFGGGTKVEIK 108


RESULT 2
Q9UL86
ID   Q9UL86      PRELIMINARY;      PRT;   109 AA.
AC   Q9UL86;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Myosin-reactive immunoglobulin kappa chain variable region
DE   (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP    EQUENCE FROM N.A.
RX    EDLINE=98277139; PubMed=9614934;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
DR   EMBL; AF035028; AAD56264.1; -.
DR   HSSP; P80362; 1WTL.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER       1       1
FT   NON_TER     109     109
SQ   SEQUENCE   109 AA;  11928 MW;  243325F72C7DAC83 CRC64;

  Query Match             89.2%;  Score 505;  DB 4;  Length 109;
  Best Local Similarity   91.7%;  Pred. No. 1.9e-47;
  Matches   99;  Conservative    2;  Mismatches    7;  Indels    0;  Gaps    0;

Qy       1 EIVLTQSPGTLSLSPGERATLSCRASQSVGSSYLAWYQQKPGQAPRLLIYGAFSRATGIP 60
           |||||||||||| |||||||||||||| ||||||||||||||||||  |||||||
Db       1 EIVLTQSPGTLSLFPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGTSSRATGIP 60

Qy      61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPWTFGQGTKVEIK 108
           |||||||| |||||||||||||||||||||||| :||| ||||:||
Db      61 DRFSGSGSETDFTLTISRLEPEDFAVYYCQQYGSSIFTFGPGTKVDIK 108


RES.  3
Q9UL83
ID   Q9UL83      PRELIMINARY;      PRT;   108 AA.
AC   Q9UL83;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Myosin-reactive immunoglobulin light chain variable region
DE   (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98277139; PubMed=9614934;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
DR   EMBL; AF035031; AAD56267.1; -.
DR   HSSP; P80362; 1WTL.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER       1       1
FT   NON_TER     108     108
SQ   SEQUENCE   108 AA;  11834 MW;  9F9C5A92EBA96EEA CRC64;

  Query Match             77.3%;  Score 437.5;  DB 4;  Length 108;
  Best Local Similarity   81.5%;  Pred. No. 4.2e-40;
  Matches   88;  Conservative    8;  Mismatches   11;  Indels    1;  Gaps    1;

Qy       1 EIVLTQSPGTLSLSPGERATLSCRASQSVGSSYLAWYQQKPGQAPRLLIYGAFSRATGIP 60
           |||:|||| |||:|||||||||||||||| || |||||||||||||||| | :||||||
Db       1 EIVMTQSPATLSVSPGERATLSCRASQSV-SSNLAWYQQKPGQAPRLLIYCASTRATGIP 59

Qy      61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPWTFGQGTKVEIK 108
           |||||||||:|||||| |: ||||||||| | : |:||| ||||:||
Db      60 ARFSGSGSGTEFTLTISSLQFEDFAVYYCQHYNNWPFTFGPGTKVDIK 107


RESULT 4
Q9UL85
ID   Q9UL85      PRELIMINARY;      PRT;   109 AA.
AC   Q9UL85;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Myosin-reactive immunoglobulin kappa chain variable region
DE   (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98277139; PubMed=9614934;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
DR   EMBL; AF035029; AAD56265.1; -.
DR   HSSP; P80362; 1WTL.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER       1       1
FT   NON_TER     109     109
SQ   SEQUENCE   109 AA;  11761 MW;  FB1E43E7C7AFACCC CRC64;

  Query Match             76.5%;  Score 433;  DB 4;  Length 109;
  Best Local Similarity   80.7%;  Pred. No. 1.3e-39;
  Matches   88;  Conservative    8;  Mismatches   11;  Indels    2;  Gaps    2;

Qy       1 EIVLTQSPGTLSLSPGERATLSCRASQSVGSSYLAWYQQKPGQAPRLLIYGAFSRATGIP 60
           |||:|||| |||:|||||||||| ||||: || |||||||||||||||||| :|||||||
Db       1 EIVMTQSPATLSVSPGERATLSCWASQSI-SSNLAWYQQKPGQAPRLLIYGASTRATGIP 59

Qy      61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGS-SPWTFGQGTKVEIK 108
           |||||||||:|||||| |: ||||:|||| |   | ||| |||||||
Db      60 ARFSGSGSGTEFTLTISSLQSEDFAIYHCQQYNSWPPLTFGGGTKVEIK 108


RESULT 5
Q9UL77
ID   Q9UL77      PRELIMINARY;      PRT;   108 AA.
AC   Q9UL77;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Myosin-reactive immunoglobulin light chain variable region
DE   (Fragment).
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GenCore version 5.1.4_p5_4578

OM protein - protein search, using sw model

Run on: April 16, 2003, 17:13:59 ; Search time 110.653 Seconds
(without alignments)
201.108 Million cell updates/sec

Title: US-09-644-668A-7
Perfect score: 566
Sequence: 1 EIVLTQSPGTLSLSPGERAT.....CQQYGSSPWTFGQGTKVEIK 108

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_21:*
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3: sp_fungi:*
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5: sp_invertebrate:*
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7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	524	92.6	109	4	Q9UL78	Q9ul78 homo sapien
2	505	89.2	109	4	Q9UL86	Q9ul86 homo sapien
3	437.5	77.3	108	4	Q9UL83	Q9ul83 homo sapien
4	433	76.5	109	4	Q9UL85	Q9ul85 homo sapien
5	404.5	71.5	108	4	Q9UL77	Q9ul77 homo sapien
6	398.5	70.4	108	4	Q9UL79	Q9ul79 homo sapien
7	381.5	67.4	108	4	Q9UL70	Q9ul70 homo sapien
8	381	67.3	107	4	Q96SA9	Q96sa9 homo sapien
9	362	64.0	107	4	Q9UL81	Q9ul81 homo sapien
10	359	63.4	238	11	Q99M37	Q99m37 mus musculu
11	357.5	63.2	111	11	Q920E9	Q920e9 mus musculu
12	352	62.2	106	5	Q9U410	Q9u410 schistosoma
13	351.5	62.1	109	11	Q920E6	Q920e6 mus musculu
14	348.5	61.6	114	4	Q9UL80	Q9ul80 homo sapien
15	347.5	61.4	108	11	Q8VIJ0	Q8vij0 mus musculu
16	347	61.3	134	11	Q8VDD0	Q8vdd0 mus musculu
17	346	61.1	238	11	Q8VCI6	Q8vci6 mus musculu
18	344.5	60.9	107	11	Q9ERZ9	Q9erz9 mus musculu
19	342	60.4	235	11	Q91W12	Q91w12 mus musculu
20	341.5	60.3	298	11	Q9QYF0	Q9qyf0 mus musculu
21	340.5	60.2	116	4	Q96PF6	Q96pf6 homo sapien
22	340.5	60.2	234	11	Q8VCP0	Q8vcp0 mus musculu
23	339.5	60.0	233	11	Q91WS9	Q91ws9 mus musculu
24	339	59.9	239	4	Q8TCD0	Q8tcd0 homo sapien
25	338	59.7	239	11	Q8VC55	Q8vc55 mus musculu
26	337.5	59.6	214	11	Q9R1A5	Q9r1a5 mus musculu
27	335.5	59.3	234	11	Q8R062	Q8r062 mus musculu
28	333.5	58.9	99	11	Q9JL74	Q9jl74 mus musculu
29	328.5	58.0	103	11	Q9JL80	Q9jl80 mus musculu
30	327	57.8	104	11	Q9JL82	Q9jl82 mus musculu
31	323.5	57.2	107	11	Q9JL84	Q9jl84 mus musculu
32	320.5	56.6	101	11	Q9JL78	Q9jl78 mus musculu
33	320.5	56.6	234	11	Q91WF8	Q91wf8 mus musculu
34	315.5	55.7	127	11	Q925S9	Q925s9 mus musculu
35	311.5	55.0	97	11	Q9JL76	Q9jl76 mus musculu
36	284	50.2	241	11	Q921A6	Q921a6 mus musculu
37	276.5	48.9	109	6	Q9N0W5	Q9n0w5 oryctolagus
38	270	47.7	237	4	Q8WUK4	Q8wuk4 homo sapien
39	270	47.7	237	4	Q8WTU6	Q8wtu6 homo sapien
40	265	46.8	233	4	Q8TBC9	Q8tbc9 homo sapien
41	263.5	46.6	234	11	Q8R028	Q8r028 mus musculu
42	259.5	45.8	236	4	Q96E61	Q96e61 homo sapien
43	247.5	43.7	112	4	Q96JD1	Q96jd1 homo sapien
44	243	42.9	108	4	Q96SB0	Q96sb0 homo sapien
45	241	42.6	110	4	Q8TE63	Q8te63 homo sapien

ALIGNMENTS

RESULT 1
Q9UL78
ID Q9UL78 PRELIMINARY; PRT; 109 AA.
AC Q9UL78;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035036; AAD56272.1; -.
DR HSSP; P80362; 1WTL.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGv; 1.
FT NON_TER 1 1
FT NON_TER 109 109
SQ SEQUENCE 109 AA; 11646 MW; 5F675C52EC7EE197 CRC64;

Query Match 92.6%; Score 524; DB 4; Length 109;
Best Local Similarity 95.4%; Pred. No. 1.6e-49;
Matches 103; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 EIVLTQSPGTLSLSPGERATLSCRASQSVGSSYLAWYQQKPGQAPRLLIYGAFSRATGIP 60
||||||||||||||||||||||||||| |||||||||||||||||||||||| |||||||
Db 1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60

```
RESULT 2
KV3L_HUMAN
ID   KV3L_HUMAN     STANDARD;      PRT;   129 AA.
AC   P18135;
DT   01-NOV-1990 (Rel. 16, Created)
DT   01-NOV-1990 (Rel. 16, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-III region HAH precursor.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=88171307; PubMed=3127527;
RA   Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;
RT   "Autoantibody-associated kappa light chain variable region gene
RT   expressed in chronic lymphocytic leukemia with little or no somatic
RT   mutation. Implications for etiology and immunotherapy.";
RL   J. Exp. Med. 167:840-852(1988).
CC   -!- DISEASE: THE PROTEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN M
CC       AUTOANTIBODIES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCYTIC
CC       LEUKEMIA.
DR   PIR; PL0022; K3HUHA.
DR   HSSP; P80362; 1WTL.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL        1     20
FT   CHAIN        21    129       IG KAPPA CHAIN V-III REGION HAH.
FT   DOMAIN       21     43       FRAMEWORK-1.
FT   DOMAIN       44     55       COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN       56     70       FRAMEWORK-2.
FT   DOMAIN       71     77       COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN       78    109       FRAMEWORK-3.
FT   DOMAIN      110    118       COMPLEMENTARITY-DETERMINING-3.
FT   DOMAIN      119    129       JK1 SEGMENT.
FT   DISULFID     43    109       BY SIMILARITY.
FT   NON_TER     129    129
SQ   SEQUENCE   129 AA;  14073 MW;  D3C55292772774D0 CRC64;

  Query Match             94.5%;  Score 535;  DB 1;  Length 129;
  Best Local Similarity   96.3%;  Pred. No. 2.1e-48;
  Matches  104;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 EIVLTQSPGTLSLSPGERATLSCRASQSVGSSYLAWYQQKPGQAPRLLIYGAFSRATGIP 60
           |||||||||||||||||||||||||||||| |||||||||||||||||||||| |||||||
Db      21 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 80

Qy      61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPWTFGQGTKVEIK 108
           |||||||||||||||||||||||||||||:|| ||||||||||
Db      81 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGTSPRTFGQGTKVEIK 128


RESULT 3
KV3B_HUMAN
ID   KV3B_HUMAN     STANDARD;      PRT;   109 AA.
AC   P01620;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-III region SIE.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=82046598; PubMed=6794615;
RA   Andrews D.W., Capra J.D.;
RT   "Amino acid sequence of the variable regions of light chains from two
RT   idiotypically cross-reactive human IgM anti-gamma-globulins of the Wa
RT   group.";
RL   Biochemistry 20:5816-5822(1981).
CC   -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
CC       GLOBULIN ACTIVITY.
DR   PIR; A01892; K3HUSI.
DR   HSSP; P80362; 1WTL.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region.
FT   DISULFID     23     89       BY SIMILARITY.
FT   NON_TER     109    109
SQ   SEQUENCE   109 AA;  11775 MW;  7689C3ECD646FFB4 CRC64;

  Query Match             93.5%;  Score 529;  DB 1;  Length 109;
  Best Local Similarity   94.4%;  Pred. No. 7.2e-48;
  Matches  102;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 EIVLTQSPGTLSLSPGERATLSCRASQSVGSSYLAWYQQKPGQAPRLLIYGAFSRATGIP 60
           |||||||||||||||||||||||||||||| :|||||||||||||||||||| |||||||
Db       1 EIVLTQSPGTLSLSPGERATLSCRASQSVSNSYLAWYQQKPGQAPRLLIYGASSRATGIP 60

Qy      61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPWTFGQGTKVEIK 108
           |||||||||||||||||||||:||||||||||||||| |||||:|||||
Db      61 DRFSGSGSGTDFTLTISRLEPDDFAVYYCQQYGSSPQTFGQGSKVEIK 108


RESULT 4
KV3D_HUMAN
ID   KV3D_HUMAN     STANDARD;      PRT;   109 AA.
AC   P01622;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-III region TI.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=72188439; PubMed=5027703;
RA   Suter L., Barnikol H.U., Watanabe S., Hilschmann N.;
RT   "Rule of antibody structure. The primary structure of a monoclonal
RT   immunoglobulin L-chain of kappa-type, subgroup 3 (Bence-Jones protein
RT   Ti). IV. The complete amino acid sequence and its significance for
RT   the mechanism of antibody production.";
RL   Hoppe-Seyler's Z. Physiol. Chem. 353:189-208(1972).
CC   -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC   -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR   PIR; A01895; K3HUTI.
DR   HSSP; P80362; 1WTL.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Bence-Jones protein.
FT   DISULFID     23     89       BY SIMILARITY.
FT   NON_TER     109    109
SQ   SEQUENCE   109 AA;  11788 MW;  8C35058CDC7749BC CRC64;

  Query Match             91.9%;  Score 520;  DB 1;  Length 109;
  Best Local Similarity   93.5%;  Pred. No. 6.1e-47;
  Matches  101;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1 EIVLTQSPGTLSLSPGERATLSCRASQSVGSSYLAWYQQKPGQAPRLLIYGAFSRATGIP 60
           |||||||||||||||||||||||||||||| :|:|||||||||||||||| | |||||||
Db       1 EIVLTQSPGTLSLSPGERATLSCRASQSVSNSFLAWYQQKPGQAPRLLIYVASSRATGIP 60

Qy      61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPWTFGQGTKVEIK 108
           |||||||||||||||||||||||||||||||||||| |||||||||:|
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GenCore version 5.1.4_p5_4578

OM protein - protein search, using sw model

Run on: April 16, 2003, 16:57:42 ; Search time 21.2211 Seconds
(without alignments)
211.085 Million cell updates/sec

Title: US-09-644-668A-7
Perfect score: 566
Sequence: 1 EIVLTQSPGTLSLSPGERAT.....CQQYGSSPWTFGQGTKVEIK 108

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	546	96.5	129	1	KV3M_HUMAN	P18136 homo sapien
2	535	94.5	129	1	KV3L_HUMAN	P18135 homo sapien
3	529	93.5	109	1	KV3B_HUMAN	P01620 homo sapien
4	520	91.9	109	1	KV3D_HUMAN	P01622 homo sapien
5	515	91.0	109	1	KV3E_HUMAN	P01623 homo sapien
6	503	88.9	108	1	KV3A_HUMAN	P01619 homo sapien
7	500	88.3	109	1	KV3G_HUMAN	P04206 homo sapien
8	469	82.9	100	1	KV3C_HUMAN	P01621 homo sapien
9	466.5	82.4	128	1	KV3K_HUMAN	P06311 homo sapien
10	460	81.3	129	1	KV3H_HUMAN	P04207 homo sapien
11	452	79.9	109	1	KV3F_HUMAN	P01624 homo sapien
12	419.5	74.1	115	1	KV3I_HUMAN	P04433 homo sapien
13	417.5	73.8	134	1	KV4C_HUMAN	P06314 homo sapien
14	414	73.1	116	1	KV3J_HUMAN	P04434 homo sapien
15	408.5	72.2	114	1	KV4A_HUMAN	P01625 homo sapien
16	392.5	69.3	108	1	KV1M_HUMAN	P01605 homo sapien
17	392	69.3	133	1	KV4B_HUMAN	P06313 homo sapien
18	391.5	69.2	108	1	KV1R_HUMAN	P01610 homo sapien
19	390.5	69.0	108	1	KV1H_HUMAN	P01600 homo sapien
20	383.5	67.8	108	1	KV1V_HUMAN	P04430 homo sapien
21	383.5	67.8	111	1	KV3O_MOUSE	P01667 mus musculu
22	380.5	67.2	108	1	KV1F_HUMAN	P01598 homo sapien
23	380.5	67.2	108	1	KV1K_HUMAN	P01603 homo sapien
24	378.5	66.9	111	1	KV3Q_MOUSE	P01669 mus musculu
25	377.5	66.7	108	1	KV1B_HUMAN	P01594 homo sapien
26	375.5	66.3	111	1	KV3M_MOUSE	P01665 mus musculu
27	374.5	66.2	108	1	KV1Y_HUMAN	P80362 homo sapien
28	372.5	65.8	108	1	KV1L_HUMAN	P01604 homo sapien
29	372	65.7	107	1	KV1D_HUMAN	P01596 homo sapien
30	371.5	65.6	111	1	KV3L_MOUSE	P01664 mus musculu
31	369.5	65.3	111	1	KV3N_MOUSE	P01666 mus musculu
32	369	65.2	110	1	KV3P_MOUSE	P01668 mus musculu
33	368.5	65.1	108	1	KV1Q_HUMAN	P01609 homo sapien
34	368.5	65.1	129	1	KV1W_HUMAN	P04431 homo sapien
35	368.5	65.1	131	1	KV3I_MOUSE	P01661 mus musculu
36	367.5	64.9	108	1	KV1E_HUMAN	P01597 homo sapien
37	367.5	64.9	108	1	KV1N_HUMAN	P01606 homo sapien
38	366.5	64.8	111	1	KV3H_MOUSE	P01660 mus musculu
39	366	64.7	113	1	KV2D_HUMAN	P01617 homo sapien
40	365	64.5	117	1	KV2E_HUMAN	P06309 homo sapien
41	363.5	64.2	111	1	KV3A_MOUSE	P01654 mus musculu
42	363.5	64.2	111	1	KV3C_MOUSE	P01656 mus musculu
43	361.5	63.9	108	1	KV1O_HUMAN	P01607 homo sapien
44	360.5	63.7	112	1	KV3G_MOUSE	P01659 mus musculu
45	359.5	63.5	111	1	KV3J_MOUSE	P01662 mus musculu

ALIGNMENTS

RESULT 1
KV3M_HUMAN
ID KV3M_HUMAN STANDARD; PRT; 129 AA.
AC P18136;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region HIC precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88171307; PubMed=3127527;
RA Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;
RT "Autoantibody-associated kappa light chain variable region gene
RT expressed in chronic lymphocytic leukemia with little or no somatic
RT mutation. Implications for etiology and immunotherapy.";
RL J. Exp. Med. 167:840-852(1988).
CC -!- DISEASE: THE PROTEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN M
CC AUTOANTIBODIES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCYTIC
CC LEUKEMIA.
DR PIR; PL0021; K3HUHI.
DR HSSP; P80362; 1WTL.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGv; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 129 IG KAPPA CHAIN V-III REGION HIC.
FT DOMAIN 21 43 FRAMEWORK-1.
FT DOMAIN 44 55 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 56 70 FRAMEWORK-2.
FT DOMAIN 71 77 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 78 109 FRAMEWORK-3.
FT DOMAIN 110 118 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 119 129 JK1 SEGMENT.
FT DISULFID 43 109 BY SIMILARITY.
FT NON_TER 129 129
SQ SEQUENCE 129 AA; 14070 MW; 7395528EA2BB74D6 CRC64;

Query Match 96.5%; Score 546; DB 1; Length 129;
Best Local Similarity 97.2%; Pred. No. 1.5e-49;
Matches 105; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy      1 EIVLTQSPGTLSLSPGERATLSCRASQSVGSSYLAWYQQKPGQAPRLLIYGAFSRATGIP 60
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Db     21 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 80

Qy     61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPWTFGQGTKVEIK 108
          |||||||||||||||||||| |||||||||||||||||||||||||||
Db     81 DRFSGSGSGTDFTLTISRLEPXDFAVYYCQQYGSSPWTFGQGTKVEIK 128
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C;Keywords: autoantibody; chronic lymphocytic leukemia; heterotetramer; immunoglobulin
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-129/Product: Ig kappa chain V-III region (Hic) #status predicted <MAT>
F;21-117/Region: V segment
F;36-111/Domain: immunoglobulin homology <IMM>
F;44-55/Region: complementarity-determining 1
F;71-77/Region: complementarity-determining 2
F;110-117/Region: complementarity-determining 3
F;118-129/Region: J segment (JK1)
F;43-109/Disulfide bonds: #status predicted

  Query Match             96.5%;  Score 546;  DB 1;  Length 129;
  Best Local Similarity   97.2%;  Pred. No. 8.6e-39;
  Matches  105;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 EIVLTQSPGTLSLSPGERATLSCRASQSVGSSYLAWYQQKPGQAPRLLIYGAFSRATGIP 60
           |||||||||||||||||||||||||||| |||||||||||||||||||||| |||||||
Db      21 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 80

Qy      61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPWTFGQGTKVEIK 108
           |||||||||||||||||| |||||||||||||||||||||||||||||
Db      81 DRFSGSGSGTDFTLTISRLEPXDFAVYYCQQYGSSPWTFGQGTKVEIK 128


RESULT 3
H30601
Ig kappa chain V-III region (Gar and Flo) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 21-Jan-2000
C;Accession: H30601; E30601
R;Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Solc
J. Immunol. 142, 3158-3163, 1989
A;Title: Structural and idiotypic characterization of the L chains of human IgM autoanti
A;Reference number: A30601; MUID:89215279; PMID:2496160
A;Accession: H30601
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-109 <GON1>
A;Accession: E30601
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-109 <GON2>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-91/Domain: immunoglobulin homology <IMM>

  Query Match             95.4%;  Score 540;  DB 2;  Length 109;
  Best Local Similarity   96.3%;  Pred. No. 2.3e-38;
  Matches  104;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 EIVLTQSPGTLSLSPGERATLSCRASQSVGSSYLAWYQQKPGQAPRLLIYGAFSRATGIP 60
           |||||||||||||||||||||||||||| |||||||||||||||||||||| |||||||
Db       1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60

Qy      61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPWTFGQGTKVEIK 108
           |||||||||||||||||||||||||||||||||:|||||||:|||
Db      61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPYTFGQGTKLEIK 108


RESULT 4
B30601
Ig kappa chain V-III region (Glo) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 21-Jan-2000
C;Accession: B30601
R;Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Solc
J. Immunol. 142, 3158-3163, 1989
A;Title: Structural and idiotypic characterization of the L chains of human IgM autoanti
A;Reference number: A30601; MUID:89215279; PMID:2496160
A;Accession: B30601
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-109 <GON>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-91/Domain: immunoglobulin homology <IMM>

  Query Match             95.2%;  Score 539;  DB 2;  Length 109;
  Best Local Similarity   97.2%;  Pred. No. 2.8e-38;
  Matches  105;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 EIVLTQSPGTLSLSPGERATLSCRASQSVGSSYLAWYQQKPGQAPRLLIYGAFSRATGIP 60
           |||||||||||||||||||||||||||| |||||||||||||||||||||| |||||||
Db       1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60

Qy      61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPWTFGQGTKVEIK 108
           |||||||||||||||||||||||||||||||||| ||||||||||
Db      61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPLTFGQGTKVEIK 108


RESULT 5
D30601
Ig kappa chain V-III region (Cur) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 21-Jan-2000
C;Accession: D30601
R;Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Solc
J. Immunol. 142, 3158-3163, 1989
A;Title: Structural and idiotypic characterization of the L chains of human IgM autoanti
A;Reference number: A30601; MUID:89215279; PMID:2496160
A;Accession: D30601
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-109 <GON>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-91/Domain: immunoglobulin homology <IMM>

  Query Match             95.1%;  Score 538;  DB 2;  Length 109;
  Best Local Similarity   97.2%;  Pred. No. 3.4e-38;
  Matches  105;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 EIVLTQSPGTLSLSPGERATLSCRASQSVGSSYLAWYQQKPGQAPRLLIYGAFSRATGIP 60
           |||||||||||||||||||||||||||| |||||||||||||||||||||| |||||||
Db       1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60

Qy      61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPWTFGQGTKVEIK 108
           |||||||||||||||||||||||||||||||||| ||||||||||
Db      61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPRTFGQGTKVEIK 108


RESULT 6
C30601
Ig kappa chain V-III region (Pay) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 21-Jan-2000
C;Accession: C30601
R;Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Solc
J. Immunol. 142, 3158-3163, 1989
A;Title: Structural and idiotypic characterization of the L chains of human IgM autoanti
A;Reference number: A30601; MUID:89215279; PMID:2496160
A;Accession: C30601
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-109 <GON>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-91/Domain: immunoglobulin homology <IMM>

  Query Match             94.7%;  Score 536;  DB 2;  Length 109;
  Best Local Similarity   96.3%;  Pred. No. 5e-38;
  Matches  104;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 EIVLTQSPGTLSLSPGERATLSCRASQSVGSSYLAWYQQKPGQAPRLLIYGAFSRATGIP 60
           |||||||||||||||||||||||||||| |||||||:|||||||||||| |||||||
Db       1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQRPGQAPRLLIYGASSRATGIP 60
```

GenCore version 5.1.4_p5_4578

OM protein - protein search, using sw model

Run on: April 16, 2003, 17:11:36 ; Search time 33.3474 Seconds
(without alignments)
311.344 Million cell updates/sec

Title: US-09-644-668A-7
Perfect score: 566
Sequence: 1 EIVLTQSPGTLSLSPGERAT.....CQQYGSSPWTFGQGTKVEIK 108

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	549	97.0	108	2	C30608	Ig kappa chain V-I
2	546	96.5	129	1	K3HUHI	Ig kappa chain pre
3	540	95.4	109	2	H30601	Ig kappa chain V-I
4	539	95.2	109	2	B30601	Ig kappa chain V-I
5	538	95.1	109	2	D30601	Ig kappa chain V-I
6	536	94.7	109	2	C30601	Ig kappa chain V-I
7	535	94.5	129	1	K3HUHA	Ig kappa chain pre
8	533	94.2	109	2	G30601	Ig kappa chain V-I
9	532	94.0	109	2	PH0963	Ig kappa chain V r
10	532	94.0	109	2	P30607	Ig kappa chain V-I
11	531	93.8	109	2	A30608	Ig kappa chain V-I
12	531	93.8	129	2	S49532	anti-Sm antibody V
13	530	93.6	129	2	S46369	IG light chain var
14	530	93.6	134	2	S38643	Ig kappa chain V r
15	529	93.5	109	1	K3HUSI	Ig kappa chain V-I
16	528.5	93.4	114	2	S46375	Ig kappa chain V-J
17	525	92.8	107	2	PH0965	Ig kappa chain V r
18	525	92.8	109	2	G30607	Ig kappa chain V-I
19	524	92.6	109	2	P30601	Ig kappa chain V-I
20	524	92.6	128	2	S20636	Ig kappa chain V r
21	520	91.9	109	1	K3HUTI	Ig kappa chain V-I
22	515	91.0	109	1	K3HUWL	Ig kappa chain V-I
23	515	91.0	110	2	S20635	Ig kappa chain V r
24	513	90.6	108	2	B30608	Ig kappa chain V-I
25	513	90.6	121	2	S40327	Ig kappa chain - h
26	510.5	90.2	110	2	E30607	Ig kappa chain V-I
27	510	90.1	109	2	F44151	Ig kappa chain V r
28	509	89.9	124	2	S20633	Ig kappa chain - h
29	508.5	89.8	108	2	H44151	Ig kappa chain V r
30	506	89.4	129	2	A32274	Ig kappa chain pre
31	503	88.9	108	1	K3HUB6	Ig kappa chain V-I
32	503	88.9	215	2	JE0242	Ig kappa chain NIG
33	502	88.7	130	2	S20637	Ig kappa chain V r
34	501.5	88.6	110	2	S44120	Ig kappa chain V-J
35	500	88.3	109	1	K3HUGO	Ig kappa chain V-I
36	500	88.3	118	2	T03036	Ig light chain - h
37	499.5	88.3	108	2	E30609	Ig kappa chain V-I
38	497	87.8	109	2	S47181	Ig kappa chain - h
39	495.5	87.5	104	2	PH0964	Ig kappa chain V r
40	495.5	87.5	129	2	S40325	Ig kappa chain - h
41	486.5	86.0	111	2	S23628	Ig kappa chain V r
42	485	85.7	96	2	A30601	Ig kappa chain V-I
43	485	85.7	116	2	B27594	Ig kappa chain pre
44	485	85.7	215	2	A23746	Ig kappa chain V-I
45	483	85.3	108	2	S33988	Ig kappa chain V r

ALIGNMENTS

RESULT 1
C30608
Ig kappa chain V-III region (Pie) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 21-Jan-2000
C;Accession: C30608
R;Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; S
J. Immunol. 142, 3158-3163, 1989
A;Title: Structural and idiotypic characterization of the L chains of human IgM autoa
A;Reference number: A30601; MUID:89215279; PMID:2496160
A;Accession: C30608
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-108 <GON>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-91/Domain: immunoglobulin homology <IMM>

Query Match 97.0%; Score 549; DB 2; Length 108;
Best Local Similarity 97.2%; Pred. No. 4.1e-39;
Matches 105; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```
Qy       1 EIVLTQSPGTLSLSPGERATLSCRASQSVGSSYLAWYQQKPGQAPRLLIYGAFSRATGIP 60
           |||||||||||||||||||||||||||| |||||||||||||||||||| |||||||
Db       1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60

Qy      61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPWTFGQGTKVEIK 108
           ||||||||||||||||||||||||||||||||||||||||||||:|||
Db      61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPWTFGQGTKLEIK 108
```

RESULT 2
K3HUHI
Ig kappa chain precursor V-III region (Hic) - human
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 21-Jan-2000
C;Accession: PL0021
R;Kipps, T.J.; Tomhave, E.; Chen, P.P.; Carson, D.A.
J. Exp. Med. 167, 840-852, 1988
A;Title: Autoantibody-associated kappa light chain variable region gene expressed in c
A;Reference number: PL0021; MUID:88171307; PMID:3127527
A;Accession: PL0021
A;Molecule type: mRNA
A;Residues: 1-129 <KIP>
C;Comment: The protein is one of the surface immunoglobulin M autoantibodies expressed
C;Genetics:
A;Gene: GDB:IGKV3
A;Cross-references: GDB:136266
A;Map position: 2p12-2p11
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (k
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into
C;Superfamily: immunoglobulin V region; immunoglobulin homology

OM protein - protein search, using sw model

Run on: April 16, 2003, 17:11:36 ; Search time 2.1614 Seconds
(without alignments)
311.344 Million cell updates/sec

Title: US-09-644-668A-29
Perfect score: 34
Sequence: 1 GAFSRAT 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

To number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	31	91.2	165	2	S08641	hypothetical prote
2	31	91.2	228	2	S32563	homeotic protein H
3	31	91.2	603	2	E84744	hypothetical prote
	30	88.2	72	2	T17585	hypothetical prote
	30	88.2	185	2	AE2388	glutathione S-tran
	30	88.2	2352	2	T43431	alpha-glucan synth
7	29	85.3	200	2	T46222	hypothetical prote
8	29	85.3	307	2	C75584	hypothetical prote
9	29	85.3	396	1	YTEC32	tetracycline resis
10	29	85.3	752	2	G82798	hypothetical prote
11	29	85.3	1084	2	G71329	hypothetical prote
12	29	85.3	1461	2	B70588	probable polyketid
13	28	82.4	131	2	S40328	Ig kappa chain - h
14	28	82.4	173	2	C95850	hypothetical prote
15	28	82.4	316	2	F71338	probable ribose/ga
16	28	82.4	361	2	AD1079	Glucosamine-fructo
17	27	79.4	164	2	AD0813	ethanolamine utili
18	27	79.4	199	2	AB3585	hypothetical prote
19	27	79.4	209	2	JC7239	peroxiredoxin V -
20	27	79.4	223	2	S73367	hypothetical prote
21	27	79.4	309	2	AI2378	periplasmic phosph
22	27	79.4	311	2	F70184	ribose/galactose A
23	27	79.4	420	2	AH3015	hemolysin [importe
24	27	79.4	425	2	G98268	hemolysin (AF21204
25	27	79.4	2067	2	A42854	probable spindle p
26	26	76.5	34	2	H30607	Ig kappa chain V-I
27	26	76.5	54	2	S40381	Ig kappa chain V-I
28	26	76.5	54	2	A25521	Ig kappa chain V r
29	26	76.5	62	2	I30601	Ig kappa chain V-I
30	26	76.5	83	2	I30607	Ig kappa chain V-I
31	26	76.5	87	2	S16843	Ig kappa chain V r
32	26	76.5	87	2	S16823	Ig kappa chain V r
33	26	76.5	89	2	S34096	Ig kappa chain V r
34	26	76.5	91	2	S37520	Ig kappa chain V r
35	26	76.5	91	2	S67940	Ig kappa chain V r
36	26	76.5	92	2	S37524	Ig kappa chain V r
37	26	76.5	92	2	S37513	Ig kappa chain V r
38	26	76.5	92	2	S37519	Ig kappa chain V r
39	26	76.5	92	2	S37517	Ig kappa chain V r
40	26	76.5	92	2	S37514	Ig kappa chain V r
41	26	76.5	92	2	S37510	Ig kappa chain V r
42	26	76.5	92	2	S37518	Ig kappa chain V r
43	26	76.5	93	2	S37526	Ig kappa chain V r
44	26	76.5	93	2	S37528	Ig kappa chain V r
45	26	76.5	96	2	A30601	Ig kappa chain V-I

ALIGNMENTS

RESULT 1
S08641
hypothetical protein 2 - zebra fish
C;Species: Brachydanio rerio (zebra fish)
C;Date: 21-Nov-1993 #sequence_revision 26-May-1995 #text_change 15-Oct-1999
C;Accession: S08641
R;Njolstad, P.R.; Molven, A.; Apold, J.; Fjose, A.
EMBO J. 9, 515-524, 1990
A;Title: The zebrafish homeobox gene hox-2.2: transcription unit, potential regulatory r
A;Reference number: S08639; MUID:90151628; PMID:1968004
A;Accession: S08641
A;Status: preliminary; translation not shown
A;Molecule type: DNA
A;Residues: 1-165 <NJO>
A;Cross-references: EMBL:X17267
C;Superfamily: unassigned homeobox proteins; homeobox homology
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation

Query Match 91.2%; Score 31; DB 2; Length 165;
Best Local Similarity 85.7%; Pred. No. 8.1;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAFSRAT 7
||:||||
Db 72 GAYSRAT 78

RESULT 2
S32563
homeotic protein Hox-B6 - zebra fish
N;Alternate names: homeotic protein Hox 2.2
C;Species: Brachydanio rerio (zebra fish)
C;Date: 08-Dec-1993 #sequence_revision 26-May-1995 #text_change 24-Sep-1999
C;Accession: S32563; S08642; S25594
R;Molven, A.; Hordvik, I.; Njolstad, P.R.
Biochim. Biophys. Acta 1173, 102-106, 1993
A;Title: Sequence analysis of the zebrafish hox-B5/B6 region.
A;Reference number: S32563; MUID:93250038; PMID:8097929
A;Accession: S32563
A;Molecule type: DNA
A;Residues: 1-228 <MOL>
A;Cross-references: EMBL:X68248; NID:g62535; PIDN:CAA48319.1; PID:g62536
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1992
A;Note: only a small part of the coding sequence given
A;Note: only a small part of the translation is shown
R;Njolstad, P.R.; Molven, A.; Apold, J.; Fjose, A.
EMBO J. 9, 515-524, 1990
A;Title: The zebrafish homeobox gene hox-2.2: transcription unit, potential regulatory r
A;Reference number: S08639; MUID:90151628; PMID:1968004
A;Accession: S08642
A;Molecule type: DNA
A;Residues: 1-228 <NJO>

A;Cross-references: EMBL:X17267; NID:g62530; PIDN:CAA35171.1; PID:g313688
C;Genetics:
A;Gene: Hox-B6; Hox 2.2
A;Introns: 144/1
C;Superfamily: unassigned homeobox proteins; homeobox homology
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;151-207/Domain: homeobox homology <HOX>

Query Match 91.2%; Score 31; DB 2; Length 228;
Best Local Similarity 85.7%; Pred. No. 11;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAFSRAT 7
||:||||
Db 64 GAYSRAT 70

RESULT 3
E84744
hypothetical protein At2g33360 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Accession: E84744
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L. euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: E84744
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-603 <STO>
A;Cross-references: GB:AE002093; NID:g2459419; PIDN:AAB80654.1; GSPDB:GN00139
C;Genetics:
A;Gene: At2g33360
A;Map position: 2

Query Match 91.2%; Score 31; DB 2; Length 603;
Best Local Similarity 85.7%; Pred. No. 29;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAFSRAT 7
|:|||||
Db 64 GSFSRAT 70

RESULT 4
T1
hypothetical protein a95R - Chlorella virus PBCV-1
C;Species: Chlorella virus PBCV-1
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T17585
R;Graves, M.V.; Van Etten, J.L.
submitted to the EMBL Data Library, May 1999
A;Reference number: Z18806
A;Accession: T17585
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-72 <GRA>
A;Cross-references: EMBL:U42580; NID:g4028896; PIDN:AAC96463.1
A;Experimental source: specific host Chlorella strain NC64A
C;Genetics:
A;Gene: a95R

Query Match 88.2%; Score 30; DB 2; Length 72;
Best Local Similarity 85.7%; Pred. No. 6.2;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAFSRAT 7
|:|||||:
Db 36 GAFSRAS 42

RESULT 5
AE2388
glutathione S-transferase [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp.
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002
C;Accession: AE2388
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Irig Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium
A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AE2388
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-185 <KUR>
A;Cross-references: GB:BA000019; PIDN:BAB76360.1; PID:g17133798; GSPDB:GN00179
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: alr4661
C;Superfamily: hypothetical protein b0838

Query Match 88.2%; Score 30; DB 2; Length 185;
Best Local Similarity 85.7%; Pred. No. 16;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAFSRAT 7
||||||:
Db 7 GAFSRAS 13

RESULT 6
T43431
alpha-glucan synthase (EC 2.4.1.-) mok12 - fission yeast (Schizosaccharomyces pombe)
N;Alternate names: morphological/kinase-inhibitor supersensitive protein mok12
C;Species: Schizosaccharomyces pombe
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jan-2000
C;Accession: T43431
R;Katayama, S.; Toda, T.
submitted to the EMBL Data Library, October 1998
A;Description: Fission yeast alpha-glucan synthase Mok1 localizes closely with actin
A;Reference number: Z22509
A;Accession: T43431
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-2352 <KAT>
A;Cross-references: EMBL:AB018381; PIDN:BAA76558.1
A;Experimental source: strain h- 972
C;Genetics:
A;Gene: mok12
C;Function:
A;Description: involved in cell morphogenesis interdependently of the actin cytoskele
C;Keywords: glycosyltransferase; hexosyltransferase; transmembrane protein

Query Match 88.2%; Score 30; DB 2; Length 2352;
Best Local Similarity 85.7%; Pred. No. 1.9e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAFSRAT 7
|||||:|
Db 1114 GAFSRVT 1120

RESULT 7
T46222
hypothetical protein T9C5.40 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 28-Jul-2000
C;Accession: T46222
R;Rieger, M.; Gabel, C.; Mueller-Auer, S.; Schaefer, M.; Zipp, M.; Mewes, H.W.; Lemcke
submitted to the Protein Sequence Database, December 1999
A;Reference number: Z23026

GenCore version 5.1.4_p5_4578

OM protein - protein search, using sw model

Run on: April 16, 2003, 16:57:42 ; Search time 1.37544 Seconds
(without alignments)
211.085 Million cell updates/sec

Title: US-09-644-668A-29
Perfect score: 34
Sequence: 1 GAFSRAT 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

To number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID		Description
1	31	91.2	228	1	HXB6_BRARE	P15861	brachydanio
2	30	88.2	2352	1	MOKC_SCHPO	Q9uul4	schizosacch
3	29	85.3	396	1	TCR3_ECOLI	P02981	escherichia
4	28	82.4	683	1	BGH3_PIG	O11780	sus scrofa
5	27	79.4	164	1	EUTK_SALTY	Q9zfu8	salmonella
6	27	79.4	210	1	PDX5_MOUSE	P99029	mus musculu
7	27	79.4	223	1	YB13_MYCPN	P75449	mycoplasma
8	27	79.4	513	1	DMP1_HUMAN	Q13316	homo sapien
9	27	79.4	514	1	MURE_RALSO	Q8xvi2	ralstonia s
10	27	79.4	2067	1	BIMB_EMENI	P33144	emericella
11	26	76.5	100	1	KV3C_HUMAN	P01621	homo sapien
12	26	76.5	106	1	YFUS_PYRWO	P29085	pyrococcus
13	26	76.5	109	1	KV3B_HUMAN	P01620	homo sapien
14	26	76.5	109	1	KV3E_HUMAN	P01623	homo sapien
15	26	76.5	109	1	KV3G_HUMAN	P04206	homo sapien
16	26	76.5	123	1	SVS5_RAT	P04812	rattus norv
17	26	76.5	129	1	KV3L_HUMAN	P18135	homo sapien
18	26	76.5	129	1	KV3M_HUMAN	P18136	homo sapien
19	26	76.5	188	1	SP21_STIAU	Q06823	stigmatella
20	26	76.5	235	1	UL03_HSV11	P10187	herpes simp
21	26	76.5	243	1	AGI6_TRYBB	Q26768	trypanosoma
22	26	76.5	251	1	TPIS_PSEAE	Q9hv51	pseudomonas
23	26	76.5	286	1	PLA2_TREMA	Q9kwx0	treponema m
24	26	76.5	304	1	YAPC_ECOLI	P30864	escherichia
25	26	76.5	326	1	Y883_PYRHO	O58613	pyrococcus
26	26	76.5	380	1	FOS_HUMAN	P01100	homo sapien
27	26	76.5	381	1	FOS_CRIGR	Q9z2q8	cricetulus
28	26	76.5	381	1	FOS_MESAU	O88479	mesocricetu
29	26	76.5	388	1	METB_MYCTU	O53427	mycobacteri
30	26	76.5	463	1	DNAA_PROS9	Q9s487	prochloroco
31	26	76.5	466	1	VL2_HPV52	P36763	human papil
32	26	76.5	477	1	VL2_HPV42	P27235	human papil
33	26	76.5	513	1	FLAB_HELPY	Q07911	helicobacte
34	26	76.5	572	1	BLRO_MYRVE	Q12737	myrothecium
35	26	76.5	916	1	MUTS_RHIME	P56883	rhizobium m
36	26	76.5	933	1	PRGR_HUMAN	P06401	homo sapien
37	26	76.5	1088	1	PIGO_HUMAN	Q8teq8	homo sapien
38	26	76.5	1333	1	YN99_YEAST	P53756	saccharomyc
39	26	76.5	1374	1	VCAP_HSV11	P06491	herpes simp
40	26	76.5	4349	1	FAT2_HUMAN	Q9nyq8	homo sapien
41	26	76.5	4351	1	FAT2_RAT	O88277	rattus norv
42	25	73.5	108	1	CYC_EISFO	P00030	eisenia foe
43	25	73.5	125	1	YFBJ_SALTI	Q8z537	salmonella
44	25	73.5	125	1	YFBJ_SALTY	Q8znf0	salmonella
45	25	73.5	163	1	PIN1_HUMAN	Q13526	homo sapien

ALIGNMENTS

RESULT 1
HXB6_BRARE
ID HXB6_BRARE STANDARD; PRT; 228 AA.
AC P15861;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Homeobox protein Hox-B6 (ZF-22).
GN HOXB6 OR HOXB6A OR HOX-B6 OR ZF-22.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=90151628; PubMed=1968004;
RA Njolstad P.R., Molven A., Apold J., Fjose A.;
RT "The zebrafish homeobox gene hox-2.2: transcription unit, potential
RT regulatory regions and in situ localization of transcripts.";
RL EMBO J. 9:515-524(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=93250038; PubMed=8097929;
RA Molven A., Hordvik I., Njolstad P.R.;
RT "Sequence analysis of the zebrafish hox-B5/B6 region.";
RL Biochim. Biophys. Acta 1173:102-106(1993).
CC -!- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF
CC A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH
CC SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- SIMILARITY: BELONGS TO THE ANTP HOMEOBOX FAMILY.
CC ---

CC ---
DR EMBL; X17267; CAA35171.1; -.
DR EMBL; X68248; CAA48319.1; -.
DR PIR; S08642; S08642.
DR PIR; S25594; S25594.
DR PIR; S32563; S32563.
DR HSSP; P02833; 1HOM.
DR TRANSFAC; T03664; -.
DR ZFIN; ZDB-GENE-990415-106; hoxb6a.
DR InterPro; IPR001827; Antennapedia.
DR InterPro; IPR001356; Homeobox.
DR Pfam; PF00046; homeobox; 1.
DR PRINTS; PR00025; ANTENNAPEDIA.
DR PRINTS; PR00024; HOMEOBOX.
DR ProDom; PD000010; Homeobox; 1.

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DR   SMART; SM00389; HOX; 1.
DR   PROSITE; PS00027; HOMEOBOX_1; 1.
DR   PROSITE; PS50071; HOMEOBOX_2; 1.
DR   PROSITE; PS00032; ANTENNAPEDIA; 1.
KW   Homeobox; DNA-binding; Developmental protein; Nuclear protein;
KW   Transcription regulation.
FT   DOMAIN      132    137       ANTP-TYPE HEXAPEPTIDE.
FT   DNA_BIND    150    209       HOMEOBOX.
FT   DOMAIN      220    224       POLY-GLU.
SQ   SEQUENCE   228 AA;  26088 MW;  4AC1B6C545B8668D CRC64;

  Query Match             91.2%;  Score 31;  DB 1;  Length 228;
  Best Local Similarity   85.7%;  Pred. No. 5.1;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GAFSRAT 7
             ||:||||
Db      64 GAYSRAT 70


RE     2
MOK_SCHPO
ID   MOKC_SCHPO     STANDARD;      PRT;  2352 AA.
AC   Q9UUL4; O13605;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Cell wall alpha-1,3-glucan synthase mok12 (EC 2.4.1.183).
GN   MOK12 OR SPBC32H8.13C OR PI011.
OS   Schizosaccharomyces pombe (Fission yeast).
OC   Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC   Schizosaccharomycetales; Schizosaccharomycetaceae;
OC   Schizosaccharomyces.
OX   NCBI_TaxID=4896;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=972;
RA   Katayama S., Dai H., Arellano M., Perez P., Toda T.;
RT   "Fission yeast alpha-glucan synthase Mok1 localizes closely with actin
RT   and play a role essential for cell morphogenesis and protein kinase C
RT   function.";
RL   Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=972;
RX   MEDLINE=20089027; PubMed=10620777;
RA   Machida M., Yamazaki S., Kunihiro S., Tanaka T., Kushida N., Jinno K.,
RA   Haikawa Y., Yamazaki J., Yamamoto S., Sekine M., Oguchi A., Nagai Y.,
RA   Sakai M., Aoki K., Ogura K., Kudoh Y., Kikuchi H., Zhang M.Q.,
RA   Yanagida M.;
RT   "A 38 kb segment containing the cdc2 gene from the left arm of fission
RT   yeast chromosome II: sequence analysis and characterization of the
RT   genomic DNA and cDNAs encoded on the segment.";
RL   Yeast 16:71-80(2000).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=972;
RX   MEDLINE=21848401; PubMed=11859360;
RA   Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA   Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA   Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA   Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA   Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA   Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA   James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA   Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA   Oliver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch E.,
RA   Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA   Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA   Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA   Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA   Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA   Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
RA   Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA   Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA   Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA   Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA   Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA   Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA   Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA   Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA   Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RT   "The genome sequence of Schizosaccharomyces pombe.";
RL   Nature 415:871-880(2002).
CC   -!- CATALYTIC ACTIVITY: UDP-glucose + {alpha-D-glucosyl-(1,3)}(N) =
CC       UDP + {alpha-D-glucosyl-(1,3)}(N+1).
CC   -!- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 1.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; AB018381; BAA76558.1; -.
DR   EMBL; AB004534; BAA21388.1; ALT_INIT.
DR   EMBL; AL590971; CAC37503.1; -.
DR   InterPro; IPR000461; Alpha_amylase.
DR   InterPro; IPR001296; Glycos_transf_1.
DR   Pfam; PF00128; alpha-amylase; 1.
DR   Pfam; PF00534; Glycos_transf_1; 1.
KW   Cell wall; Transferase; Glycosyltransferase.
SQ   SEQUENCE   2352 AA;  266561 MW;  78ADF9C2F7140BBA CRC64;

  Query Match             88.2%;  Score 30;  DB 1;  Length 2352;
  Best Local Similarity   85.7%;  Pred. No. 79;
  Matches    6;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 GAFSRAT 7
             ||||| |
Db    1114 GAFSRVT 1120


RESULT 3
TCR3_ECOLI
ID   TCR3_ECOLI     STANDARD;      PRT;   396 AA.
AC   P02981;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-DEC-1998 (Rel. 37, Last annotation update)
DE   Tetracycline resistance protein, class C (TETA(C)).
GN   TETA.
OS   Escherichia coli.
OG   Plasmid pBR322.
OC   Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC   Escherichia.
OX   NCBI_TaxID=562;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=80002802; PubMed=383387;
RA   Sutcliffe J.G.;
RT   "Complete nucleotide sequence of the Escherichia coli plasmid
RT   pBR322.";
RL   Cold Spring Harb. Symp. Quant. Biol. 43:77-90(1979).
RN   [2]
RP   REVISIONS, AND IDENTIFICATION OF PROTEIN.
RX   MEDLINE=83117828; PubMed=6337373;
RA   Livneh Z.;
RT   "Directed mutagenesis method for analysis of mutagen specificity:
RT   application to ultraviolet-induced mutagenesis.";
RL   Proc. Natl. Acad. Sci. U.S.A. 80:237-241(1983).
RN   [3]
RP   REVISIONS, AND IDENTIFICATION OF PROTEIN.
RX   MEDLINE=83263146; PubMed=6307828;
```

GenCore version 5.1.4_p5_4578

OM protein - protein search, using sw model

Run on: April 16, 2003, 17:13:59 ; Search time 7.17193 Seconds
(without alignments)
201.108 Million cell updates/sec

Title: US-09-644-668A-29
Perfect score: 34
Sequence: 1 GAFSRAT 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

To number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_21:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	31	91.2	85	12	Q8QPU3	Q8qpu3 tomato infe
2	31	91.2	603	10	O22787	O22787 arabidopsis
3	30	88.2	72	12	Q84416	Q84416 paramecium
4	30	88.2	164	11	Q9CVB3	Q9cvb3 mus musculu
5	30	88.2	185	16	Q8YNA6	Q8yna6 anabaena sp
6	30	88.2	195	17	Q9HKH3	Q9hkh3 thermoplasm
7	29	85.3	200	10	Q9S7F8	Q9s7f8 arabidopsis
8	29	85.3	307	16	Q9RYL0	Q9ryl0 deinococcus
9	29	85.3	340	2	Q9WWU8	Q9wwu8 pseudomonas
10	29	85.3	354	11	Q9QZA9	Q9qza9 mus musculu
11	29	85.3	359	4	O60759	O60759 homo sapien
12	29	85.3	359	11	Q91VY6	Q91vy6 mus musculu
13	29	85.3	396	2	Q939B6	Q939b6 aeromonas s
14	29	85.3	396	2	Q91UU6	Q91uu6 escherichia
15	29	85.3	671	2	O85671	O85671 pantoea agg
16	29	85.3	671	2	Q47867	Q47867 pantoea agg
17	29	85.3	719	16	Q8XWU4	Q8xwu4 ralstonia s
18	29	85.3	734	3	Q8WZU0	Q8wzu0 neurospora
19	29	85.3	752	16	Q9PFZ5	Q9pfz5 xylella fas
20	29	85.3	864	10	Q9LWH2	Q9lwh2 oryza sativ
21	29	85.3	1084	16	O83423	O83423 treponema p
22	29	85.3	1298	12	Q9WRL9	Q9wrl9 macaca mula
23	29	85.3	1298	12	Q9J2G9	Q9j2g9 macaca mula
24	29	85.3	1461	16	O05819	O05819 mycobacteri
25	29	85.3	1750	2	Q9RFK5	Q9rfk5 stigmatella
26	28	82.4	61	12	P89262	P89262 xestia c-ni
27	28	82.4	93	6	Q95KM1	Q95km1 canis famil
28	28	82.4	173	16	Q92X95	Q92x95 rhizobium m
29	28	82.4	185	17	Q97AG3	Q97ag3 thermoplasm
30	28	82.4	270	4	Q9HBL3	Q9hbl3 homo sapien
31	28	82.4	275	12	Q8QND9	Q8qnd9 ectocarpus
32	28	82.4	316	16	O83343	O83343 treponema p
33	28	82.4	322	3	Q9C2G7	Q9c2g7 neurospora
34	28	82.4	360	16	Q9KYZ9	Q9kyz9 streptomyce
35	28	82.4	361	16	Q8YAS8	Q8yas8 listeria mo
36	28	82.4	382	2	P96101	P96101 thiobacillu
37	28	82.4	425	4	Q96G50	Q96g50 homo sapien
38	28	82.4	478	2	O32600	O32600 pantoea agg
39	28	82.4	545	4	Q96PW7	Q96pw7 homo sapien
40	28	82.4	701	16	Q98MT5	Q98mt5 rhizobium l
41	28	82.4	707	4	Q96KH1	Q96kh1 homo sapien
42	28	82.4	707	4	Q96CT2	Q96ct2 homo sapien
43	28	82.4	749	11	Q9CY92	Q9cy92 mus musculu
44	28	82.4	786	4	Q9HAW5	Q9haw5 homo sapien
45	28	82.4	791	4	Q96KG8	Q96kg8 homo sapien

ALIGNMENTS

RESULT 1
Q8QPU3
ID Q8QPU3 PRELIMINARY; PRT; 85 AA.
AC Q8QPU3;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Putative AC4 protein.
GN AC4.
OS Tomato infectious yellows virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=172393;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MG-BI1;
RA Ribeiro S.G., Ambrozevicius L.P., de Avila A.C., Calegario R.F.,
RA Fernandes J.J., Lima M.F., Mello R.N., Rocha H., Zerbini F.M.;
RT "Distribution and genetic diversity of tomato-infecting geminiviruses
RT in Brazil.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AY049208; AAL82834.1; -.
SQ SEQUENCE 85 AA; 9571 MW; 910BB5394CD829A3 CRC64;

Query Match 91.2%; Score 31; DB 12; Length 85;
Best Local Similarity 85.7%; Pred. No. 13;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAFSRAT 7
|||||:|
Db 61 GAFSRST 67

RESULT 2
O22787
ID O22787 PRELIMINARY; PRT; 603 AA.
AC O22787;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

```
DE   At2g33360 protein.
GN   AT2G33360.
OS   Arabidopsis thaliana (Mouse-ear cress).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX   NCBI_TaxID=3702;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CV. COLUMBIA;
RX   MEDLINE=20083487; PubMed=10617197;
RA   Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA   Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
RA   Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
RA   Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E.,
RA   Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
RA   Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,
RA   Salzberg S.L., Fraser C.M., Venter J.C.;
RT   "Sequence and analysis of chromosome 2 of the plant Arabidopsis
RT   thaliana.";
RL   Nature 402:761-768(1999).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CV. COLUMBIA;
RA   Lin X.;
RL   Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AC002332; AAB80654.1; -.
SQ   SEQUENCE   603 AA;  66507 MW;  613A6A4863FC7462 CRC64;

  Query Match           91.2%;  Score 31;  DB 10;  Length 603;
  Best Local Similarity  85.7%;  Pred. No. 1e+02;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GAFSRAT 7
           |:||||
Db      64 GSFSRAT 70


RESULT 3
Q84416
ID   Q84416      PRELIMINARY;      PRT;    72 AA.
AC   Q84416;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   A95R protein.
GN   A95R.
OS   Paramecium bursaria chlorella virus 1 (PBCV-1).
OC   Viruses; dsDNA viruses, no RNA stage; Phycodnaviridae; Chlorovirus.
OX   NCBI_TaxID=10506;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=95407089; PubMed=7676624;
RA   Li Y., Lu Z., Burbank D.E., Kutish G.F., Rock D.L., Van Etten J.L.;
RT   "Analysis of 43 kb of the Chlorella virus PBCV-1 330-kb genome: map
RT   positions 45 to 88.";
RL   Virology 212:134-150(1995).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20013326; PubMed=10544099;
RA   Kaiser A., Vollmert M., Tholl D., Graves M.V., Gurnon J.R., Xing W.,
RA   Lisec A.D., Nickerson K.W., Van Etten J.L.;
RT   "Chlorella virus PBCV-1 encodes a functional homospermidine
RT   synthase.";
RL   Virology 263:254-262(1999).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20478054; PubMed=11021991;
RA   Sun L., Gurnon J.R., Adams B.J., Graves M.V., Van Etten J.L.;
RT   "Characterization of a beta-1,3-glucanase encoded by chlorella virus
RT   PBCV-1.";
RL   Virology 276:27-36(2000).
RN   [4]
RP   SEQUENCE FROM N.A.
RA   Van Etten J.L.;
RL   Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   SEQUENCE FROM N.A.
RA   Van Etten J.L.;
RL   Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
RN   [6]
RP   SEQUENCE FROM N.A.
RA   Van Etten J.L.;
RL   Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
RN   [7]
RP   SEQUENCE FROM N.A.
RA   Graves M.V., Van Etten J.L.;
RL   Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
RN   [8]
RP   SEQUENCE FROM N.A.
RA   Graves M.V., Van Etten J.L.;
RL   Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
RN   [9]
RP   SEQUENCE FROM N.A.
RA   Gurnon J.R., Graves M.V., Van Etten J.L.;
RL   Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; U42580; AAC96463.1; -.
SQ   SEQUENCE   72 AA;  7701 MW;  300F8BEF3DF59CBC CRC64;

  Query Match           88.2%;  Score 30;  DB 12;  Length 72;
  Best Local Similarity  85.7%;  Pred. No. 19;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GAFSRAT 7
           ||||||:
Db      36 GAFSRAS 42


RESULT 4
Q9CVB3
ID   Q9CVB3      PRELIMINARY;      PRT;   164 AA.
AC   Q9CVB3;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   2210404M20Rik protein (Fragment).
GN   2210404M20RIK.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=STOMACH;
RX   MEDLINE=21085660; PubMed=11217851;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
DR   EMBL; AK008830; BAB25917.1; -.
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GenCore version 5.1.4_p5_4578

OM protein - protein search, using sw model

Run on: April 16, 2003, 16:56:17 ; Search time 5.55088 Seconds
(without alignments)
168.037 Million cell updates/sec

Title: US-09-644-668A-29
Perfect score: 34
Sequence: 1 GAFSRAT 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	34	100.0	7	22	AAB67494	Human light chain
2	31	91.2	112	15	AAR54279	Anti-HIV gp41 immu
3	31	91.2	112	17	AAW01324	VL of Fab, SS 41 8
4	31	91.2	112	21	AAY95174	Anti-gp41 light ch
5	31	91.2	112	21	AAY98283	Anti-gp41 light ch
6	31	91.2	356	20	AAY34471	Porphorymonas ging
7	31	91.2	491	20	AAY34347	Porphorymonas ging
8	30	88.2	43	22	ABG00976	Novel human diagno
9	29	85.3	46	22	ABG03763	Novel human diagno
10	29	85.3	51	20	AAY41354	Human secreted pro
11	29	85.3	61	22	AAU41549	Propionibacterium
12	29	85.3	177	21	AAB51685	Gene 22 human secr
13	29	85.3	177	21	AAB51686	Human secreted pro
14	29	85.3	359	22	AAB30608	Amino acid sequenc
15	29	85.3	373	22	ABG01757	Novel human diagno
16	29	85.3	396	19	AAW56695	Tetracycline resis
17	29	85.3	396	20	AAY42545	Plasmid pRZTL1, Te
18	29	85.3	396	20	AAY15383	Plasmid pRZTL1, Te
19	29	85.3	396	22	AAB50899	Protein encoded by
20	29	85.3	396	23	AAU75552	celZ integration v
21	29	85.3	415	22	ABB52991	Escherichia coli p
22	29	85.3	1298	21	AAB53204	Macaca mulatta rha
23	28	82.4	85	22	AAU53827	Propionibacterium
24	28	82.4	143	22	AAU56695	Propionibacterium
25	28	82.4	179	22	AAU53900	Propionibacterium
26	28	82.4	259	22	ABG27325	Novel human diagno
27	28	82.4	287	21	AAB35708	Human protein cont
28	28	82.4	361	23	ABB49841	Listeria monocytog
29	28	82.4	410	20	AAW93254	Human ESRP1 protei
30	28	82.4	524	21	AAB58954	Breast and ovarian
31	28	82.4	587	22	AAB74754	Human secreted pro
32	28	82.4	587	23	ABG65328	Human albumin fusi
33	28	82.4	618	22	AAB74769	Human secreted pro
34	28	82.4	675	22	AAM40778	Human polypeptide
35	28	82.4	724	23	ABB04802	LDL receptor bindi
36	28	82.4	791	22	AAE11780	Human kinase (PKIN
37	28	82.4	808	22	AAB65679	Novel protein kina
38	28	82.4	820	21	AAB43354	Human ORFX ORF3118
39	28	82.4	832	22	AAB74457	Human Traf4 bindin
40	28	82.4	924	22	AAU09958	Human cadherin-1 (
41	28	82.4	2139	22	ABB62393	Drosophila melanog
42	27	79.4	14	22	AAM97727	Human peptide #100
43	27	79.4	28	17	AAR91383	ME#1 library deriv
44	27	79.4	88	21	AAB40534	Human ORFX ORF298
45	27	79.4	95	23	ABP02653	Human ORFX protein

ALIGNMENTS

RESULT 1
AAB67494
ID AAB67494 standard; peptide; 7 AA.
XX
AC AAB67494;
XX
DT 29-MAY-2001 (first entry)
XX
DE Human light chain complementarity determining region 2 (CDR2).
XX
KW Complementarity determining region; CDR; immune response; antibody;
KW cytotoxic T lymphocyte associated antigen-4; CTLA-4; B7 ligand; cancer;
KW autoimmune disease; infectious disease; inflammation; allergy;
KW rheumatoid arthritis; myasthenia gravis; lupus erythematosus;
KW multiple sclerosis; insulin-dependent diabetes mellitus; inflammation;
KW transplant rejection; graft versus host disease.
XX
OS Homo sapiens.
XX
PN WO200114424-A2.
XX
PD 01-MAR-2001.
XX
PF 24-AUG-2000; 2000WO-US23356.
XX
PR 24-AUG-1999; 99US-0150452.
XX
PA (MEDA-) MEDAREX INC.
XX
PI Korman AJ, Halk EL, Lonberg N;
XX
DR WPI; 2001-202933/20.
XX

```
PT   Novel human sequence antibody that binds to human cytotoxic T
PT   lymphocyte associated antigen-4, useful for inducing, augmenting or
PT   prolonging immune response to antigen or for suppressing immune
PT   response in patient -
XX
PS   Claim 30; Page 99; 127pp; English.
XX
CC   AAB67490-99 and AAB67501-06 represents complementarity determining
CC   regions (CDRs) of human antibodies. The antibodies specifically bind to
CC   human cytotoxic T lymphocyte associated antigen-4 (CTLA-4). Such
CC   antibodies are used in methods for inducing, augmenting or prolonging
CC   an immune response to an antigen in a patient, where the antibodies
CC   block binding of human CTLA-4 to human B7 ligands. The antibodies are
CC   also useful for treating autoimmune disease in a subject caused or
CC   exacerbated by increased activity of T cells and for treating prostate
CC   cancer, melanoma or epithelial cancer. A polyvalent or polyclonal
CC   antibody preparation comprising two antibodies of the invention are
CC   useful for suppressing a immune response in a patient. They are used for
CC   treating cancer, infectious diseases and promoting beneficial autoimmune
CC   reactions for the treatment of diseases with inflammatory or allergic
CC   components. The polyvalent or polyclonal preparations are useful for
CC   treating autoimmune diseases such as rheumatoid arthritis, myasthenia
CC   gravis and lupus erythematosus, multiple sclerosis, insulin-dependent
CC   diabetes mellitus, transplant rejection, and inflammation, graft versus
CC   host disease.
XX
SQ   Sequence   7 AA;

  Query Match             100.0%;  Score 34;  DB 22;  Length 7;
  Best Local Similarity   100.0%;  Pred. No. 7.8e+05;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GAFSRAT 7
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Db       1 GAFSRAT 7
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RESULT 2
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ID   AAR54279 standard; protein; 112 AA.
XX
AC   AAR54279;
XX
DT   10-NOV-1994  (first entry)
XX
DE   Anti-HIV gp41 immunoglobulin light chain V region clone SS 41 8.
XX
KW   Human immunodeficiency virus; HIV1; glycoprotein gp41; epitope;
KW   neutralisation; monoclonal antibody; light chain; variable region;
KW   framework region; complementarity determining region.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
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FT                   /label= FR1
FT   Region          24..35
FT                   /label= CDR1
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FT                   /label= FR2
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FT   Region          58..89
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FT   Region          90..98
FT                   /label= CDR3
FT   Region          99..112
FT                   /label= FR4
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PN   WO9407922-A.
XX
PD   14-APR-1994.
XX
PF   30-SEP-1993;   93WO-US09328.
XX
PR   30-SEP-1992;   92US-0954148.
XX
PA   (SCRI ) SCRIPPS RES INST.
XX
PI   Barbas CF,  Burton DR,  Lerner RA;
XX
DR   WPI; 1994-135516/16.
XX
PT   New human monoclonal antibodies neutralising HIV - react with
PT   gp120 or gp41 and nucleic acid encoding them, useful for in vivo
PT   or in vitro diagnosis and for passive immuno-therapy
XX
PS   Claim 11; Page 218; 248pp; English.
XX
CC   Lymphocyte mRNA was converted to cDNA and subjected to PCR
CC   amplification using primers specific for heavy and light chain
CC   variable regions. The amplification products were inserted into a
CC   dicistronic vector to produce a library of fragments. E.coli XL1
CC   Blue cells were transformed with the library. Filamentous phage were
CC   produced which expressed the MAb regions on their surface. Panning
CC   with gp120 and gp41 resulted in the recovery of immunoreactive
CC   clones. The light chain VL region sequence AAR54279 neutralises HIV1
CC   gp41.
XX
SQ   Sequence   112 AA;

  Query Match             91.2%;  Score 31;  DB 15;  Length 112;
  Best Local Similarity   85.7%;  Pred. No. 17;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GAFSRAT 7
           ||:||||
Db      51 GAYSRAT 57
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RESULT 3
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ID   AAW01324 standard; Protein; 112 AA.
XX
AC   AAW01324;
XX
DT   29-JAN-1997  (first entry)
XX
DE   VL of Fab, SS 41 8, binds to HIV gp41.
XX
KW   Heavy chain; light chain; variable region; VH; monoclonal antibody;
KW   MAb; HIV; human immunodeficiency virus; glycoprotein; gp120; clone;
KW   virus infectivity assay; precursor gp160; immunocompetence; human;
KW   anti-HIV antibody; detection; HIV infection.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
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FT                   /label= FR1
FT   Region          24..35
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PN   WO9602273-A1.
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PD   01-FEB-1996.
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GenCore version 5.1.4_p5_4578

OM protein - protein search, using sw model

Run on: April 16, 2003, 17:21:54 ; Search time 2.06316 Seconds
(without alignments)
256.547 Million cell updates/sec

Title: US-09-644-668A-29
Perfect score: 34
Sequence: 1 GAFSRAT 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 288829 seqs, 75613885 residues

Tc number of hits satisfying chosen parameters: 288829

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	28	82.4	524	9	US-10-102-806-662	Sequence 662, App
3	28	82.4	924	10	US-09-838-529-2	Sequence 2, Appli
4	27	79.4	151	10	US-09-893-737-240	Sequence 240, App
5	27	79.4	427	9	US-09-975-719-107	Sequence 107, App
6	26	76.5	7	10	US-09-828-708-45	Sequence 45, Appl
7	26	76.5	7	10	US-09-828-708-47	Sequence 47, Appl
8	26	76.5	7	10	US-09-828-708-48	Sequence 48, Appl
9	26	76.5	7	10	US-09-828-708-49	Sequence 49, Appl
10	26	76.5	72	9	US-09-796-692-2362	Sequence 2362, Ap
11	26	76.5	74	9	US-10-125-687-23	Sequence 23, Appl
12	26	76.5	74	12	US-10-025-687-23	Sequence 23, Appl
13	26	76.5	96	9	US-10-194-975-82	Sequence 82, Appl
14	26	76.5	104	10	US-09-828-708-6	Sequence 6, Appli
15	26	76.5	105	10	US-09-828-708-3	Sequence 3, Appli
16	26	76.5	105	10	US-09-828-708-5	Sequence 5, Appli
17	26	76.5	105	10	US-09-828-708-7	Sequence 7, Appli
18	26	76.5	107	8	US-08-844-215-8	Sequence 8, Appli
19	26	76.5	108	9	US-09-848-798-178	Sequence 178, App
20	26	76.5	109	9	US-10-125-687-10	Sequence 10, Appl
21	26	76.5	109	12	US-10-025-687-10	Sequence 10, Appl
22	26	76.5	110	9	US-10-001-934-40	Sequence 40, Appl
23	26	76.5	202	10	US-09-815-242-10606	Sequence 10606, A
24	26	76.5	236	10	US-09-859-053-34	Sequence 34, Appl
25	26	76.5	236	10	US-09-859-053-38	Sequence 38, Appl
26	26	76.5	245	9	US-09-880-748-1896	Sequence 1896, Ap
27	26	76.5	246	9	US-09-880-748-1264	Sequence 1264, Ap
28	26	76.5	249	9	US-09-880-748-1035	Sequence 1035, Ap
29	26	76.5	251	9	US-09-880-748-1219	Sequence 1219, Ap
30	26	76.5	251	10	US-09-815-242-12053	Sequence 12053, A
31	26	76.5	253	9	US-09-880-748-1499	Sequence 1499, Ap
32	26	76.5	303	9	US-10-063-547-166	Sequence 166, App
33	26	76.5	303	9	US-10-174-590-562	Sequence 562, App
34	26	76.5	303	9	US-10-176-758-562	Sequence 562, App
35	26	76.5	303	9	US-10-063-616-166	Sequence 166, App
36	26	76.5	303	9	US-10-175-737-562	Sequence 562, App
37	26	76.5	303	9	US-10-063-502-166	Sequence 166, App
38	26	76.5	303	9	US-10-173-706-562	Sequence 562, App
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41	26	76.5	303	9	US-10-176-482-562	Sequence 562, App
42	26	76.5	303	9	US-10-176-757-562	Sequence 562, App
43	26	76.5	303	9	US-10-176-913-562	Sequence 562, App
44	26	76.5	303	9	US-10-180-552-562	Sequence 562, App
45	26	76.5	303	9	US-10-180-557-562	Sequence 562, App

ALIGNMENTS

RESULT 1
US-10-029-180-138
; Sequence 138, Application US/10029180
; Publication No. US20020182708A1
; GENERAL INFORMATION:
; APPLICANT: Cali, Brian M.
; APPLICANT: Holtzman, Doug
; APPLICANT: Madden, Kevin T.
; APPLICANT: Milna, G. Todd
; APPLICANT: Sherman, Amir
; APPLICANT: Silva, Jeffry C.
; APPLICANT: Trueheart, Josh
; APPLICANT: Zhang, Lixin
; TITLE OF INVENTION: No. US20020182708A1el Regulators of Fungal Gene Expression
; FILE REFERENCE: MIC-004
; CURRENT APPLICATION NUMBER: US/10/029,180
; CURRENT FILING DATE: 2001-12-22
; PRIOR APPLICATION NUMBER: US 60/257,431
; PRIOR FILING DATE: 2000-12-22
; NUMBER OF SEQ ID NOS: 138
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 138
; LENGTH: 805
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fungal gene
US-10-029-180-138

Query Match 85.3%; Score 29; DB 9; Length 805;
Best Local Similarity 85.7%; Pred. No. 1.4e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAFSRAT 7
||:||||
Db 797 GAWSRAT 803

RESULT 2
US-10-102-806-662
; Sequence 662, Application US/10102806
; Publication No. US20030054421A1

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; GENERAL INFORMATION:
;  APPLICANT: Rosen et al.
;  TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
;  FILE REFERENCE: PA103P1C1
;  CURRENT APPLICATION NUMBER: US/10/102,806
;  CURRENT FILING DATE:  2002-03-22
;  PRIOR APPLICATION NUMBER: 09/925,298
;  PRIOR FILING DATE: 2001-08-10
;  PRIOR APPLICATION NUMBER: PCT/US00/05881
;  PRIOR FILING DATE: 2000-03-08
;  PRIOR APPLICATION NUMBER: 60/124,270
;  PRIOR FILING DATE: 1999-03-12
;  NUMBER OF SEQ ID NOS: 846
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 662
;   LENGTH: 524
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (124)
;   OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
;   NAME/KEY: SITE
;   LOCATION: (191)
;   OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-102-806-662

  Query Match             82.4%;  Score 28;  DB 9;  Length 524;
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  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 AFSRAT 7
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Db     422 AFSRAT 427


RESULT 3
US-09-838-529-2
; Sequence 2, Application US/09838529
; Patent No. US20020081599A1
; GENERAL INFORMATION:
;  APPLICANT: Curtis, Rory A. J.
;  TITLE OF INVENTION: 57809 AND 57798, NOVEL HUMAN CADHERIN
;  TITLE OF INVENTION:  MOLECULES AND USES THEREFOR
;  FILE REFERENCE: MNI-145
;  CURRENT APPLICATION NUMBER: US/09/838,529
;  CURRENT FILING DATE:  2001-04-18
;  PRIOR APPLICATION NUMBER: 60/198,466
;  PRIOR FILING DATE: 2000-04-18
;  NUMBER OF SEQ ID NOS: 7
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 924
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-838-529-2

  Query Match             82.4%;  Score 28;  DB 10;  Length 924;
  Best Local Similarity   71.4%;  Pred. No. 2.7e+02;
  Matches    5;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GAFSRAT 7
           |::||||
Db      33 GSYSRAT 39


RESULT 4
US-09-893-737-240
; Sequence 240, Application US/09893737
; Patent No. US20020110855A1
; GENERAL INFORMATION:
;  APPLICANT: Sheppard, Paul O.
;  APPLICANT:  Presnell, Scott R.
;  TITLE OF INVENTION: MAMMALIAN SECRETED PROTEINS
;  FILE REFERENCE: 00-41
;  CURRENT APPLICATION NUMBER: US/09/893,737
;  CURRENT FILING DATE:  2001-06-28
;  PRIOR APPLICATION NUMBER: US 60/215,446
;  PRIOR FILING DATE: 2000-06-30
;  NUMBER OF SEQ ID NOS: 329
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 240
;   LENGTH: 151
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-893-737-240

  Query Match             79.4%;  Score 27;  DB 10;  Length 151;
  Best Local Similarity   71.4%;  Pred. No. 68;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 GAFSRAT 7
           | :||||
Db     142 GVYSRAT 148


RESULT 5
US-09-975-719-107
; Sequence 107, Application US/09975719
; Publication No. US20030022349A1
; GENERAL INFORMATION:
;  APPLICANT: Ausubel, Frederick M.
;  APPLICANT:  Rahme, Laurence G.
;  TITLE OF INVENTION: VIRULENCE-ASSOCIATED NUCLEIC ACID
;  TITLE OF INVENTION:  SEQUENCES AND USES THEREOF
;  FILE REFERENCE: 00786/361003
;  CURRENT APPLICATION NUMBER: US/09/975,719
;  CURRENT FILING DATE:  2001-10-10
;  PRIOR APPLICATION NUMBER: US 09/199,637
;  PRIOR FILING DATE: 1998-11-25
;  PRIOR APPLICATION NUMBER: US 60/066,517
;  PRIOR FILING DATE: 1997-11-25
;  NUMBER OF SEQ ID NOS: 437
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 107
;   LENGTH: 427
;   TYPE: PRT
;   ORGANISM: Pseudomonas aeruginosa
US-09-975-719-107

  Query Match             79.4%;  Score 27;  DB 9;  Length 427;
  Best Local Similarity   71.4%;  Pred. No. 2e+02;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 GAFSRAT 7
           ||| :||
Db     127 GAFEKAT 133


RESULT 6
US-09-828-708-45
; Sequence 45, Application US/09828708
; Patent No. US20020146753A1
; GENERAL INFORMATION:
;  APPLICANT: Ditzel, H.
;  APPLICANT:  Burton, D.
;  APPLICANT:  Schaller, M.
;  TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their parti
;  TITLE OF INVENTION:  autoimmune disease
;  FILE REFERENCE: 1361.005US1
;  CURRENT APPLICATION NUMBER: US/09/828,708
;  CURRENT FILING DATE:  2001-09-24
;  NUMBER OF SEQ ID NOS: 123
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 45
;   LENGTH: 7
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GenCore version 5.1.4_p5_4578

OM protein - protein search, using sw model

Run on: April 16, 2003, 17:15:40 ; Search time 1.79298 Seconds
(without alignments)
114.870 Million cell updates/sec

Title: US-09-644-668A-29
Perfect score: 34
Sequence: 1 GAFSRAT 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	31	91.2	112	1	US-08-276-852-151	Sequence 151, App
2	31	91.2	112	1	US-08-899-575-151	Sequence 151, App
3	31	91.2	112	1	US-08-899-575-151	Sequence 151, App
4	31	91.2	112	5	PCT-US95-08743-151	Sequence 151, App
5	29	85.3	396	2	US-08-850-880-4	Sequence 4, Appli
6	29	85.3	396	2	US-08-944-916-4	Sequence 4, Appli
7	29	85.3	396	2	US-08-814-877-4	Sequence 4, Appli
8	29	85.3	396	4	US-09-272-432A-4	Sequence 4, Appli
9	28	82.4	724	4	US-09-562-737-25	Sequence 25, Appl
10	27	79.4	427	4	US-09-199-637A-107	Sequence 107, App
11	26	76.5	56	1	US-08-162-102C-39	Sequence 39, Appl
12	26	76.5	107	1	US-08-107-669D-14	Sequence 14, Appl
13	26	76.5	107	1	US-08-472-788A-14	Sequence 14, Appl
14	26	76.5	107	2	US-08-477-531B-14	Sequence 14, Appl
15	26	76.5	107	2	US-08-652-558-49	Sequence 49, Appl
16	26	76.5	107	2	US-08-082-842A-14	Sequence 14, Appl
17	26	76.5	108	1	US-07-634-278-86	Sequence 86, Appl
18	26	76.5	108	1	US-08-477-728-86	Sequence 86, Appl
19	26	76.5	108	1	US-08-474-040-86	Sequence 86, Appl
20	26	76.5	108	1	US-08-487-200-86	Sequence 86, Appl
21	26	76.5	108	1	US-08-488-113B-150	Sequence 150, App
22	26	76.5	108	1	US-08-477-484B-150	Sequence 150, App
23	26	76.5	108	2	US-08-646-360-150	Sequence 150, App
24	26	76.5	108	2	US-08-232-081B-42	Sequence 42, Appl
25	26	76.5	108	4	US-08-839-765-150	Sequence 150, App
26	26	76.5	108	4	US-09-136-389-150	Sequence 150, App
27	26	76.5	108	4	US-08-484-537-86	Sequence 86, Appl
28	26	76.5	108	4	US-09-240-274-178	Sequence 178, App
29	26	76.5	108	4	US-09-610-838-150	Sequence 150, App
30	26	76.5	109	1	US-08-162-102C-24	Sequence 24, Appl
31	26	76.5	109	4	US-09-025-769B-16	Sequence 16, Appl
32	26	76.5	109	5	PCT-US93-08786-24	Sequence 24, Appl
33	26	76.5	110	4	US-09-025-769B-30	Sequence 30, Appl
34	26	76.5	110	4	US-09-025-769B-47	Sequence 47, Appl
35	26	76.5	116	1	US-08-053-131-183	Sequence 183, App
36	26	76.5	116	2	US-08-096-762-183	Sequence 183, App
37	26	76.5	116	4	US-09-042-353-46	Sequence 46, Appl
38	26	76.5	116	4	US-08-758-417A-311	Sequence 311, App
39	26	76.5	117	1	US-08-466-033-164	Sequence 164, App
40	26	76.5	117	2	US-08-444-733-164	Sequence 164, App
41	26	76.5	117	2	US-08-464-134-164	Sequence 164, App
42	26	76.5	117	2	US-08-461-361-164	Sequence 164, App
43	26	76.5	117	2	US-08-485-910-164	Sequence 164, App
44	26	76.5	129	2	US-08-480-774A-4	Sequence 4, Appli
45	26	76.5	232	1	US-08-638-911A-33	Sequence 33, Appl

ALIGNMENTS

```
RESULT 1
US-08-276-852-151
; Sequence 151, Application US/08276852
; Patent No. 5652138
;  GENERAL INFORMATION:
;    APPLICANT:  Burton, Dennis R
;    APPLICANT:  Barbas, Carlos F
;    APPLICANT:  Lerner, Richard A
;    TITLE OF INVENTION:  HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
;    TITLE OF INVENTION:  TO HUMAN IMMUNODEFICIENCY VIRUS
;    NUMBER OF SEQUENCES:  170
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  The Scripps Research Institute, Office of
;      ADDRESSEE:  Patent Counsel
;      STREET:  10666 No. 5652138th Torrey Pines Road, Suite 220,
;      STREET:  Mail Drop TPC8
;      CITY:  La Jolla
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  92037
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/276,852
;      FILING DATE:  18-JUL-1994
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/178,302
;      FILING DATE:  30-SEP-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/954,148
;      FILING DATE:  30-SEP-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fitting, Thomas
;      REGISTRATION NUMBER:  34,163
;      REFERENCE/DOCKET NUMBER:  SCR1452P
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  619-554-2937
;      TELEFAX:  619-554-6312
;  INFORMATION FOR SEQ ID NO:  151:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  112 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-276-852-151
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  Query Match             91.2%;  Score 31;  DB 1;  Length 112;
  Best Local Similarity   85.7%;  Pred. No. 4.6;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GAFSRAT 7
          ||:||||
Db     51 GAYSRAT 57


RESULT 2
US-08-899-575-151
; Sequence 151, Application US/08899575
; Patent No. 5770440
;  GENERAL INFORMATION:
;    APPLICANT:  Burton, Dennis R
;    APPLICANT:  Barbas, Carlos F
;    APPLICANT:  Lerner, Richard A
;    TITLE OF INVENTION:  HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
;    TITLE OF INVENTION:  TO HUMAN IMMUNODEFICIENCY VIRUS
;    NUMBER OF SEQUENCES:  170
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  The Scripps Research Institute, Office of
;      ADDRESSEE:  Patent Counsel
;      STREET:  10666 No. 5770440th Torrey Pines Road, Suite 220,
;      STREET:  Mail Drop TPC8
;      CITY:  La Jolla
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  92037
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/899,575
;      FILING DATE:  24-JUL-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/276,852
;      FILING DATE:  18-JUL-1994
;      APPLICATION NUMBER:  US 08/178,302
;      FILING DATE:  30-SEP-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/954,148
;      FILING DATE:  30-SEP-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fitting, Thomas
;      REGISTRATION NUMBER:  34,163
;      REFERENCE/DOCKET NUMBER:  SCR1452P
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  619-554-2937
;      TELEFAX:  619-554-6312
;  INFORMATION FOR SEQ ID NO:  151:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  112 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-899-575-151

  Query Match             91.2%;  Score 31;  DB 1;  Length 112;
  Best Local Similarity   85.7%;  Pred. No. 4.6;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GAFSRAT 7
          ||:||||
Db     51 GAYSRAT 57


RESULT 3
US-08-899-575-151
; Sequence 151, Application US/08899575
; Patent No. 5804440
;  GENERAL INFORMATION:
;    APPLICANT:  Burton, Dennis R
;    APPLICANT:  Barbas, Carlos F
;    APPLICANT:  Lerner, Richard A
;    TITLE OF INVENTION:  HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
;    TITLE OF INVENTION:  TO HUMAN IMMUNODEFICIENCY VIRUS
;    NUMBER OF SEQUENCES:  170
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  The Scripps Research Institute, Office of
;      ADDRESSEE:  Patent Counsel
;      STREET:  10666 No. 5804440th Torrey Pines Road, Suite 220,
;      STREET:  Mail Drop TPC8
;      CITY:  La Jolla
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  92037
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/899,575
;      FILING DATE:  24-JUL-1997
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/276,852
;      FILING DATE:  18-JUL-1994
;      APPLICATION NUMBER:  US 08/178,302
;      FILING DATE:  30-SEP-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/954,148
;      FILING DATE:  30-SEP-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fitting, Thomas
;      REGISTRATION NUMBER:  34,163
;      REFERENCE/DOCKET NUMBER:  SCR1452P
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  619-554-2937
;      TELEFAX:  619-554-6312
;  INFORMATION FOR SEQ ID NO:  151:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  112 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-899-575-151

  Query Match             91.2%;  Score 31;  DB 1;  Length 112;
  Best Local Similarity   85.7%;  Pred. No. 4.6;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GAFSRAT 7
          ||:||||
Db     51 GAYSRAT 57


RESULT 4
PCT-US95-08743-151
; Sequence 151, Application PC/TUS9508743
;  GENERAL INFORMATION:
;    APPLICANT:
;    TITLE OF INVENTION:  HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
;    TITLE OF INVENTION:  TO HUMAN IMMUNODEFICIENCY VIRUS
;    NUMBER OF SEQUENCES:  170
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25 (EPO)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/08743
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OM protein - protein search, using sw model

Run on: April 16, 2003, 17:11:36 ; Search time 5.24912 Seconds
(without alignments)
311.344 Million cell updates/sec

Title: US-09-644-668A-32
Perfect score: 93
Sequence: 1 FISYDGNNKYYADSVKG 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	83	89.2	98	2	S29543	Ig heavy chain V r
2	83	89.2	117	2	S36259	Ig heavy chain V r
3	83	89.2	134	2	S31688	Ig heavy chain V r
	83	89.2	135	2	S31598	Ig heavy chain V r
	83	89.2	140	2	S70442	Ig heavy chain pre
	82	88.2	94	2	PL0120	Ig heavy chain V-I
7	82	88.2	97	2	S44115	Ig heavy chain V r
8	82	88.2	98	2	PL0116	Ig heavy chain V-I
9	82	88.2	98	2	S29546	Ig heavy chain V r
10	82	88.2	109	2	PH1644	Ig heavy chain V r
11	82	88.2	109	2	PH1646	Ig heavy chain V r
12	82	88.2	111	2	PH1643	Ig heavy chain V r
13	82	88.2	111	2	PH1645	Ig heavy chain V r
14	82	88.2	113	2	S38490	Ig heavy chain - h
15	82	88.2	114	2	S46390	Ig heavy chain V r
16	82	88.2	114	2	S46392	Ig heavy chain V r
17	82	88.2	117	2	S36270	Ig heavy chain V r
18	82	88.2	118	2	S31677	Ig heavy chain V r
19	82	88.2	118	2	S31116	Ig heavy chain - h
20	82	88.2	119	2	F36005	Ig heavy chain V r
21	82	88.2	120	2	S31112	Ig heavy chain - h
22	82	88.2	121	2	S19666	Ig heavy chain V r
23	82	88.2	121	2	G36005	Ig heavy chain V r
24	82	88.2	122	2	E36005	Ig heavy chain V r
25	82	88.2	122	2	S31119	Ig heavy chain - h
26	82	88.2	123	2	S38493	Ig heavy chain - h
27	82	88.2	130	2	PL0098	Ig heavy chain pre
28	82	88.2	132	2	S31603	Ig heavy chain V r
29	82	88.2	134	2	S31679	Ig heavy chain V r
30	82	88.2	139	2	S31674	Ig heavy chain V r
31	78	83.9	76	2	S31592	Ig heavy chain V r
32	78	83.9	133	2	S31510	Ig heavy chain - h
33	77	82.8	122	1	M3HUAM	Ig heavy chain V-I
34	77	82.8	137	2	S31701	Ig heavy chain V r
35	75	80.6	108	2	PH1642	Ig heavy chain V r
36	75	80.6	114	2	S46391	Ig heavy chain V r
37	75	80.6	118	2	PH1660	Ig heavy chain V r
38	75	80.6	119	2	S31111	Ig heavy chain - h
39	75	80.6	122	2	S31117	Ig heavy chain - h
40	75	80.6	128	2	S48797	Ig heavy chain V r
41	75	80.6	133	2	A49028	Ig heavy chain V-I
42	74	79.6	110	2	S69897	Ig heavy chain V r
43	74	79.6	118	2	PH1662	Ig heavy chain V r
44	72	77.4	121	2	PH1661	Ig heavy chain V r
45	71	76.3	119	2	S37453	Ig mu chain - huma

ALIGNMENTS

RESULT 1
S29543
Ig heavy chain V region (COS 3) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 07-Jan-1994 #sequence_revision 17-Nov-1995 #text_change 23-Jul-1999
C;Accession: S29543
R;Tomlinson, M.; Walter, G.; Cook, G.P.; Winter, G.
submitted to the EMBL Data Library, October 1992
A;Reference number: S29543
A;Accession: S29543
A;Molecule type: DNA
A;Residues: 1-98 <TOM>
A;Cross-references: EMBL:Z17389; NID:g32835; PIDN:CAA78994.1; PID:g32836
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 89.2%; Score 83; DB 2; Length 98;
Best Local Similarity 88.2%; Pred. No. 9.2e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Qy      1 FISYDGNNKYYADSVKG 17
          || |||:||||||||||
Db     50 FIRYDGSNKYYADSVKG 66
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RESULT 2
S36259
Ig heavy chain V region (clone alpha-TNF-A1) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Jul-1999
C;Accession: S36259
R;Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.
EMBO J. 12, 725-734, 1993
A;Title: Human anti-self antibodies with high specificity from phage display libraries.
A;Reference number: S36256; MUID:93178448; PMID:7679990
A;Accession: S36259
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-117 <GRI>
A;Cross-references: EMBL:Z18850; NID:g33123; PIDN:CAA79302.1; PID:g939902
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 89.2%; Score 83; DB 2; Length 117;
Best Local Similarity 88.2%; Pred. No. 1.1e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Qy      1 FISYDGNNKYYADSVKG 17
          || |||:||||||||||
Db     50 FIRYDGSNKYYADSVKG 66
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RESULT 3
S31688
Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S31688
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A;Description: Mechanisms that generate human immunoglobulin diversity operate from the
A;Reference number: S31585
A;Accession: S31688
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-134 <CUI>
A;Cross-references: EMBL:Z14174; NID:g31013; PIDN:CAA78543.1; PID:g31014
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;3[illegible]14/Domain: immunoglobulin homology <IMM>

Query Match 89.2%; Score 83; DB 2; Length 134;
Best Local Similarity 88.2%; Pred. No. 1.3e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FISYDGNNKYYADSVKG 17
|| |||:||||||||||
Db 66 FIRYDGSNKYYADSVKG 82

RESULT 4
S31598
Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S31598
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A;Description: Mechanisms that generate human immunoglobulin diversity operate from the
A;Reference number: S31585
A;Accession: S31598
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-135 <CUI>
A;Cross-references: EMBL:Z14170; NID:g31001; PIDN:CAA78539.1; PID:g31002
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;3[illegible]14/Domain: immunoglobulin homology <IMM>

[illegible]y Match 89.2%; Score 83; DB 2; Length 135;
Best Local Similarity 88.2%; Pred. No. 1.3e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FISYDGNNKYYADSVKG 17
|| |||:||||||||||
Db 66 FIRYDGSNKYYADSVKG 82

RESULT 5
S70442
Ig heavy chain precursor V region (mu) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 21-Jan-2000
C;Accession: S70442
R;Cuisinier, A.M.; Fumoux, F.; Fougereau, M.; Tonnelle, C.
Mol. Immunol. 29, 1363-1373, 1992
A;Title: IgM kappa/lambda EBV human B cell clone: an early step of differentiation of fe
A;Reference number: S70442; MUID:93024508; PMID:1383695
A;Accession: S70442
A;Status: [illegible]ot compared with conceptual translation
A;Molecule [illegible]ype: mRNA
A;Residues: [illegible]-140 <CUI>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 89.2%; Score 83; DB 2; Length 140;
Best Local Similarity 88.2%; Pred. No. 1.3e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FISYDGNNKYYADSVKG 17
|| |||:||||||||||
Db 69 FIRYDGSNKYYADSVKG 85

RESULT 6
PL0120
Ig heavy chain V-III region (TD-Vo) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 16-Aug-1996
C;Accession: PL0120
R;Bird, J.; Galili, N.; Link, M.; Stites, D.; Sklar, J.
J. Exp. Med. 168, 229-245, 1988
A;Title: Continuing rearrangement but absence of somatic hypermutation in immunoglobul
A;Reference number: PL0116; MUID:88286083; PMID:2840480
A;Accession: PL0120
A;Molecule type: mRNA
A;Residues: 1-94 <BIR>
A;Experimental source: B cells from patient TD with acute lymphoblastic leukemia, ALL
A;Note: the sequence shows the V region (TD-Vo) from a nonproductive DNA rearrangement
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: acute lymphoblastic leukemia; heterotetramer; immunoglobulin
F;31-35/Region: complementarity-determining 1
F;49-65/Region: complementarity-determining 2

Query Match 88.2%; Score 82; DB 2; Length 94;
Best Local Similarity 93.8%; Pred. No. 1.3e-05;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ISYDGNNKYYADSVKG 17
|||||:||||||||||
Db 51 ISYDGSNKYYADSVKG 66

RESULT 7
S44115
Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-May-2001
C;Accession: S44115
R;Hawkins, R.E.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.
submitted to the EMBL Data Library, March 1994
A;Description: Idiotypic vaccination against human B-cell lymphoma: rescue of variable
A;Reference number: S44105
A;Accession: S44115
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-97 <HAW>
A;Cross-references: EMBL:Z31384; NID:g472969; PIDN:CAA83259.1; PID:g940526
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

Query Match 88.2%; Score 82; DB 2; Length 97;
Best Local Similarity 93.8%; Pred. No. 1.3e-05;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ISYDGNNKYYADSVKG 17
|||||:||||||||||
Db 51 ISYDGSNKYYADSVKG 66

RESULT 8
PL0116
Ig heavy chain V-III region (AW-Vx) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 23-Jul-1999
C;Accession: PL0116; S26892

GenCore version 5.1.4_p5_4578

OM protein - protein search, using sw model

Run on: April 16, 2003, 16:57:42 ; Search time 3.34035 Seconds
(without alignments)
211.085 Million cell updates/sec

Title: US-09-644-668A-32
Perfect score: 93
Sequence: 1 PISYDGNNKYYADSVKG 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

To: umber of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID		Description
1	77	82.8	122	1	HV3G_HUMAN	P01768	homo sapien
2	67	72.0	122	1	HV3H_HUMAN	P01769	homo sapien
3	66	71.0	119	1	HV3I_HUMAN	P01770	homo sapien
4	63	67.7	119	1	HV3L_HUMAN	P01773	homo sapien
5	57	61.3	116	1	HV05_CARAU	P19181	carassius a
6	54	58.1	114	1	HV3B_HUMAN	P01763	homo sapien
7	54	58.1	121	1	HV3J_HUMAN	P01771	homo sapien
	53	57.0	115	1	HV3F_HUMAN	P01767	homo sapien
	53	57.0	126	1	HV3K_HUMAN	P01772	homo sapien
	52	55.9	119	1	HV3M_HUMAN	P01774	homo sapien
11	52	55.9	119	1	HV3N_HUMAN	P01775	homo sapien
12	52	55.9	122	1	HV3A_HUMAN	P01762	homo sapien
13	50	53.8	117	1	HV3C_HUMAN	P01764	homo sapien
14	49	52.7	117	1	HV54_MOUSE	P18525	mus musculu
15	49	52.7	117	1	HV55_MOUSE	P18526	mus musculu
16	48	51.6	120	1	HV3U_HUMAN	P01782	homo sapien
17	46.5	50.0	264	1	GUNS_ERWCA	P16630	erwinia car
18	46	49.5	98	1	HV57_MOUSE	P18528	mus musculu
19	45	48.4	117	1	HV53_MOUSE	P18524	mus musculu
20	45	48.4	120	1	HV3E_HUMAN	P01766	homo sapien
21	44	47.3	97	1	HV56_MOUSE	P18527	mus musculu
22	44	47.3	116	1	HV60_MOUSE	P18531	mus musculu
23	44	47.3	780	1	TREB_YEAST	P35172	saccharomyc
24	43	46.2	116	1	HV3T_HUMAN	P01781	homo sapien
25	43	46.2	117	1	HV03_CARAU	P19180	carassius a
26	43	46.2	117	1	HV58_MOUSE	P18529	mus musculu
27	43	46.2	367	1	Y046_MYCTU	P71703	mycobacteri
28	42	45.2	136	1	HV16_MOUSE	P01783	mus musculu
29	42	45.2	229	1	Y997_HAEIN	P44090	haemophilus
30	42	45.2	261	1	NU1M_PARTE	P05513	paramecium
31	42	45.2	360	1	YJGQ_ECOLI	P39341	escherichia
32	42	45.2	473	1	6PGD_BUCAP	Q9zhd9	buchnera ap
33	42	45.2	479	1	6PGD_CHLMU	Q9pkx7	chlamydia m
34	42	45.2	480	1	6PGD_CHLTR	O84066	chlamydia t
35	42	45.2	2452	1	RPB1_PLAFD	P14248	plasmodium
36	41.5	44.6	117	1	HV02_CANFA	P01785	canis famil
37	41.5	44.6	2333	1	POLG_FMDV1	P03306	f genome po
38	41	44.1	113	1	V195_FOWPV	Q9j538	fowlpox vir
39	41	44.1	137	1	HV46_MOUSE	P01822	mus musculu
40	41	44.1	353	1	GBT2_BOVIN	P04696	bos taurus
41	41	44.1	353	1	GBT2_HUMAN	P19087	homo sapien
42	41	44.1	353	1	GBT2_MOUSE	P50149	mus musculu
43	41	44.1	385	1	T1SI_HAEIN	P71344	haemophilus
44	41	44.1	398	1	VE2_HPV63	Q07850	human papil
45	41	44.1	428	1	HEMA_CVMA5	P31615	murine coro

ALIGNMENTS

RESULT 1
HV3G_HUMAN
ID HV3G_HUMAN STANDARD; PRT; 122 AA.
AC P01768;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V-III region CAM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=81013859; PubMed=6774332;
RA Lehman D.W., Putnam F.W.;
RT "Amino acid sequence of the variable region of a human mu chain:
RT location of a possible JH segment.";
RL Proc. Natl. Acad. Sci. U.S.A. 77:3239-3243(1980).
CC -!- MISCELLANEOUS: THIS MU CHAIN WAS ISOLATED FROM THE PLASMA OF A
CC PATIENT WITH MACROGLOBULINEMIA.
DR PIR; A02051; M3HUAM.
DR HSSP; P01772; 2FB4.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGv; 1.
KW Immunoglobulin V region.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT NON_TER 122 122
SQ SEQUENCE 122 AA; 13668 MW; A42D0F17D252F1C2 CRC64;

Query Match 82.8%; Score 77; DB 1; Length 122;
Best Local Similarity 75.0%; Pred. No. 8.3e-06;
Matches 12; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

```
Qy       2 ISYDGNNKYYADSVKG 17
           |||:|::||||:||||
Db      51 ISYBGBBKYYABSVKG 66
```

RESULT 2
HV3H_HUMAN
ID HV3H_HUMAN STANDARD; PRT; 122 AA.
AC P01769;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V-III region GA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=74175307; PubMed=4208843;

```
RA   Florent G., Lehman D., Putnam F.W.;
RT   "The switch point in mu heavy chains of human IgM immunoglobulins.";
RL   Biochemistry 13:2482-2498(1974).
CC   -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S
CC       MACROGLOBULIN.
DR   PIR; A02052; M3HUGA.
DR   HSSP; P01772; 2FB4.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region.
FT   MOD_RES       1      1       PYRROLIDONE CARBOXYLIC ACID.
FT   NON_TER     122    122
SQ   SEQUENCE   122 AA;  13166 MW;  74E5B6959E84100A CRC64;

  Query Match             72.0%;  Score 67;  DB 1;  Length 122;
  Best Local Similarity   68.8%;  Pred. No. 0.00037;
  Matches   11;  Conservative    4;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2 ISYDGNNKYYADSVKG 17
           |||:|:::||| ||||
Db      51 ISYBGBBZYYAASVKG 66


RESULT 3
HV3I_HUMAN
ID   HV3I_HUMAN     STANDARD;      PRT;   119 AA.
AC   P01770;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig heavy chain V-III region NIE.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=77070269; PubMed=826475;
RA   Ponstingl H., Hilschmann N.;
RT   "The rule of antibody structure. The primary structure of a
RT   monoclonal IgG1 immunoglobulin (myeloma protein Nie). III. The
RT   chymotryptic peptides of the H-chain, alignment of the tryptic
RT   peptides and discussion of the complete structure.";
RL   Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).
RN   [2]
RP   DISULFIDE BOND.
RX   MEDLINE=77070267; PubMed=1002129;
RA   Dreker L., Schwarz J., Reichel W., Hilschmann N.;
RT   "Rule of antibody structure. The primary structure of a monoclonal
RT   IgG1 immunoglobulin (myeloma protein Nie), I: Purification and
RT   characterization of the protein, the L- and H-chains, the
RT   cyanogen bromide cleavage products, and the disulfide bridges.";
RL   Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
CC   -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG1 MYELOMA
CC       PROTEIN.
DR   PIR; A02053; G1HUNI.
DR   HSSP; P01772; 2FB4.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region.
FT   MOD_RES       1      1       PYRROLIDONE CARBOXYLIC ACID.
FT   DISULFID     22     96
FT   NON_TER     119    119
SQ   SEQUENCE   119 AA;  13242 MW;  C96935A6E55E165B CRC64;

  Query Match             71.0%;  Score 66;  DB 1;  Length 119;
  Best Local Similarity   62.5%;  Pred. No. 0.00052;
  Matches   10;  Conservative    5;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2 ISYDGNNKYYADSVKG 17
           :||:|::|:|||| |
Db      51 MSYBGBBKHYADSVNG 66


RESULT 4
HV3L_HUMAN
ID   HV3L_HUMAN     STANDARD;      PRT;   119 AA.
AC   P01773;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig heavy chain V-III region BUR.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE (MYELOMA PROTEIN BUR).
RX   MEDLINE=79151016; PubMed=107164;
RA   Putnam F.W., Liu Y.-S.V., Low T.L.K.;
RT   "Primary structure of a human IgA1 immunoglobulin. IV. Streptococcal
RT   IgA1 protease, digestion, Fab and Fc fragments, and the complete
RT   amino acid sequence of the alpha 1 heavy chain.";
RL   J. Biol. Chem. 254:2865-2874(1979).
DR   PIR; A02056; A1HUBR.
DR   HSSP; P01772; 2FB4.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Glycoprotein.
FT   MOD_RES       1      1       PYRROLIDONE CARBOXYLIC ACID.
FT   DISULFID     22     96
FT   CARBOHYD     28     28       N-LINKED (GLCNAC. . .).
FT   NON_TER     119    119
SQ   SEQUENCE   119 AA;  12981 MW;  12A709A75344D024 CRC64;

  Query Match             67.7%;  Score 63;  DB 1;  Length 119;
  Best Local Similarity   68.8%;  Pred. No. 0.0016;
  Matches   11;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2 ISYDGNNKYYADSVKG 17
           ||| |:: ||||||:|
Db      51 ISYGGSBTYYADSVRG 66


RESULT 5
HV05_CARAU
ID   HV05_CARAU     STANDARD;      PRT;   116 AA.
AC   P19181;
DT   01-NOV-1990 (Rel. 16, Created)
DT   01-NOV-1990 (Rel. 16, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig heavy chain V region 5A precursor.
OS   Carassius auratus (Goldfish).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Carassius.
OX   NCBI_TaxID=7957;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=88144476; PubMed=3125551;
RA   Wilson M.R., Middleton D., Warr G.W.;
RT   "Immunoglobulin heavy chain variable region gene evolution: structure
RT   and family relationships of two genes and a pseudogene in a teleost
RT   fish.";
RL   Proc. Natl. Acad. Sci. U.S.A. 85:1566-1570(1988).
DR   PIR; B28966; B28966.
DR   HSSP; P01772; 2FB4.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
```

GenCore version 5.1.4_p5_4578

OM protein - protein search, using sw model

Run on: April 16, 2003, 17:13:59 ; Search time 17.4175 Seconds
(without alignments)
201.108 Million cell updates/sec

Title: US-09-644-668A-32
Perfect score: 93
Sequence: 1 FISYDGNNKYYADSVKG 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

To number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_21:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	83	89.2	113	4	Q9UL90	Q9ul90 homo sapien
2	82	88.2	116	4	Q9UL93	Q9ul93 homo sapien
3	82	88.2	613	4	Q8WUK1	Q8wuk1 homo sapien
4	69	74.2	122	4	Q9UL84	Q9ul84 homo sapien
5	65	69.9	147	4	Q9Y509	Q9y509 homo sapien
6	61	65.6	118	4	Q9UL72	Q9ul72 homo sapien
7	60	64.5	95	4	Q9ULB6	Q9ulb6 homo sapien
8	60	64.5	121	4	Q9UL71	Q9ul71 homo sapien
9	54	58.1	597	4	Q96BB9	Q96bb9 homo sapien
10	50	53.8	536	5	O45994	O45994 caenorhabdi
11	49	52.7	479	11	Q91WP5	Q91wp5 mus musculu
12	48	51.6	71	7	Q9XRR6	Q9xrr6 sigmodon hi
13	48	51.6	71	7	Q9GJ71	Q9gj71 salmo trutt
14	48	51.6	486	11	Q91Z07	Q91z07 mus musculu
15	47	50.5	112	4	Q9HCC1	Q9hcc1 homo sapien
16	47	50.5	119	11	Q920E7	Q920e7 mus musculu
17	47	50.5	2203	5	Q963L8	Q96318 schistosoma
18	46	49.5	308	2	Q9S0K5	Q9s0k5 shewanella
19	46	49.5	469	2	Q9FAR9	Q9far9 shewanella
20	46	49.5	576	13	Q8QHJ1	Q8qhj1 brachydanio
21	46	49.5	609	12	Q9EMF0	Q9emf0 amsacta moo
22	45	48.4	273	16	Q92FT5	Q92ft5 listeria in
23	45	48.4	273	16	Q8YAU4	Q8yau4 listeria mo
24	45	48.4	305	17	Q97CD6	Q97cd6 thermoplasm
25	45	48.4	612	13	Q9DDC6	Q9ddc6 melanogramm
26	44	47.3	71	7	Q31366	Q31366 brachydanio
27	44	47.3	87	10	Q9AV03	Q9av03 oryza sativ
28	44	47.3	175	2	Q9LCW3	Q9lcw3 streptomyce
29	44	47.3	317	5	Q8WR58	Q8wr58 plasmodium
30	44	47.3	326	5	Q8WP98	Q8wp98 plasmodium
31	44	47.3	414	5	Q963G5	Q963g5 plasmodium
32	44	47.3	416	4	Q9NPP6	Q9npp6 homo sapien
33	44	47.3	491	5	Q963G9	Q963g9 plasmodium
34	44	47.3	574	16	Q9KTW1	Q9ktw1 vibrio chol
35	44	47.3	606	16	Q977Y3	Q977y3 clostridium
36	44	47.3	683	2	Q9L4N0	Q914n0 streptococc
37	44	47.3	735	2	Q8VP61	Q8vp61 streptococc
38	44	47.3	785	16	Q98QS3	Q98qs3 mycoplasma
39	44	47.3	1956	5	Q962L5	Q962l5 plasmodium
40	43	46.2	71	7	Q9XRR9	Q9xrr9 sigmodon hi
41	43	46.2	71	7	Q9XRR5	Q9xrr5 sigmodon hi
42	43	46.2	71	7	Q9XRR3	Q9xrr3 sigmodon hi
43	43	46.2	71	7	Q9GJD3	Q9gjd3 sigmodon hi
44	43	46.2	118	4	Q9UL91	Q9ul91 homo sapien
45	43	46.2	129	2	Q60111	Q60111 yersinia ps

ALIGNMENTS

RESULT 1
Q9UL90
ID Q9UL90 PRELIMINARY; PRT; 113 AA.
AC Q9UL90;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035024; AAD56260.1; -.
DR HSSP; P01772; 2FB4.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGv; 1.
FT NON_TER 1 1
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12437 MW; ED57FDD19086D07F CRC64;

Query Match 89.2%; Score 83; DB 4; Length 113;
Best Local Similarity 88.2%; Pred. No. 1.8e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Qy      1 FISYDGNNKYYADSVKG 17
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Db     50 FIRYDGSNKYYADSVKG 66
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RESULT 2
Q9UL93
ID   Q9UL93       PRELIMINARY;      PRT;   116 AA.
AC   Q9UL93;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Myosin-reactive immunoglobulin heavy chain variable region
DE   (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98277139; PubMed=9614934;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
DR   EMBL; AF035021; AAD56257.1; -.
DR   HSSP; P01772; 2FB4.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER       1      1
FT   NON_TER     116    116
SQ   SEQUENCE   116 AA;  12434 MW;  0DA0348154DD6061 CRC64;

  Query Match             88.2%;  Score 82;  DB 4;  Length 116;
  Best Local Similarity   93.8%;  Pred. No. 2.6e-05;
  Matches   15;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 ISYDGNNKYYADSVKG 17
           |||||:||||||||||
Db      50 ISYDGSNKYYADSVKG 65


RESULT 3
Q8WUK1
ID   Q8WUK1       PRELIMINARY;      PRT;   613 AA.
AC   Q8WUK1;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Hypothetical 67.3 kDa protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=TONSIL;
RA   Strausberg R.;
RL   Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC020240; AAH20240.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 5.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 4.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_3.
KW   Hypothetical protein.
SQ   SEQUENCE   613 AA;  67296 MW;  60C7F5950671E315 CRC64;

  Query Match             88.2%;  Score 82;  DB 4;  Length 613;
  Best Local Similarity   93.8%;  Pred. No. 0.00017;
  Matches   15;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 ISYDGNNKYYADSVKG 17
           |||||:||||||||||
Db      70 ISYDGSNKYYADSVKG 85


RESULT 4
Q9UL84
ID   Q9UL84       PRELIMINARY;      PRT;   122 AA.
AC   Q9UL84;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Myosin-reactive immunoglobulin heavy chain variable region
DE   (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98277139; PubMed=9614934;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
DR   EMBL; AF035030; AAD56266.1; -.
DR   HSSP; P01772; 2FB4.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER       1      1
FT   NON_TER     122    122
SQ   SEQUENCE   122 AA;  13579 MW;  36054D41366545B8 CRC64;

  Query Match             74.2%;  Score 69;  DB 4;  Length 122;
  Best Local Similarity   81.2%;  Pred. No. 0.003;
  Matches   13;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2 ISYDGNNKYYADSVKG 17
           || ||:||:|||||||
Db      51 ISNDGSNKFYADSVKG 66


RESULT 5
Q9Y509
ID   Q9Y509       PRELIMINARY;      PRT;   147 AA.
AC   Q9Y509;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   VH3 protein (Fragment).
GN   VH3.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96071149; PubMed=7475288;
RA   Cao J., Vescio R.A., Rettig M.B., Hong C.H., Kim A., Lee J.C.,
RA   Lichtenstein A.K., Berenson J.R.;
RT   "A CD10-positive subset of malignant cells is identified in multiple
RT   myeloma using PCR with patient-specific immunoglobulin gene primers.";
RL   Leukemia 9:1948-1953(1995).
DR   EMBL; S80860; AAD14339.1; -.
DR   HSSP; P01772; 2FB4.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
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OM protein - protein search, using sw model

Run on: April 16, 2003, 16:56:17 ; Search time 13.4807 Seconds
(without alignments)
168.037 Million cell updates/sec

Title: US-09-644-668A-32
Perfect score: 93
Sequence: 1 FISYDGNNKYYADSVKG 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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23: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	93	100.0	17	22	AAB67491	Human heavy chain
2	93	100.0	118	22	AAB67508	Light chain variab
3	93	100.0	118	22	AAB67513	Heavy chain variab
4	88	94.6	17	21	AAB39830	Anti-hIL12 antibod
5	87	93.5	17	22	AAU08361	Antibody heavy cha
6	87	93.5	220	22	AAU08384	Anti-OPGbp antibod
7	85	91.4	17	21	AAB39836	Anti-hIL12 antibod
8	85	91.4	17	21	AAB39838	Anti-hIL12 antibod
9	84	90.3	17	21	AAB39829	Anti-hIL12 antibod
10	84	90.3	17	21	AAB39833	Anti-hIL12 antibod
11	84	90.3	17	21	AAB39835	Anti-hIL12 antibod
12	84	90.3	17	21	AAB39837	Anti-hIL12 antibod
13	83	89.2	17	21	AAB39487	Anti-hIL-12 antibo
14	83	89.2	17	21	AAB39503	Anti-hIL-12 antibo
15	83	89.2	17	21	AAB39511	Anti-hIL-12 antibo
16	83	89.2	17	21	AAB39828	Anti-hIL12 antibod
17	83	89.2	17	21	AAB39832	Anti-hIL12 antibod
18	83	89.2	17	21	AAB39834	Anti-hIL12 antibod
19	83	89.2	17	21	AAB39842	Anti-hIL12 antibod
20	83	89.2	17	21	AAB39865	Anti-hIL12 antibod
21	83	89.2	17	21	AAB39871	Anti-hIL12 antibod
22	83	89.2	17	21	AAB39881	Anti-hIL12 antibod
23	83	89.2	17	22	AAB67496	Human heavy chain
24	83	89.2	98	21	AAB40123	Anti-hIL12 antibod
25	83	89.2	98	21	AAB40141	Anti-hIL12 antibod
26	83	89.2	114	21	AAB39499	Anti-hIL-12 antibo
27	83	89.2	115	21	AAB39507	Anti-hIL-12 antibo
28	83	89.2	115	21	AAB39515	Anti-hIL-12 antibo
29	83	89.2	115	21	AAB39517	Anti-IL12 antibody
30	83	89.2	115	21	AAB39519	Anti-IL12 antibody
31	83	89.2	115	21	AAB39521	Anti-IL12 antibody
32	83	89.2	115	21	AAB39523	Anti-IL12 antibody
33	83	89.2	115	21	AAB39525	Anti-IL12 antibody
34	83	89.2	115	21	AAB39527	Anti-IL12 antibody
35	83	89.2	115	21	AAB39529	Anti-IL12 antibody
36	83	89.2	115	21	AAB39531	Anti-IL12 antibody
37	83	89.2	115	21	AAB39533	Anti-IL12 antibody
38	83	89.2	115	21	AAB39535	Anti-IL12 antibody
39	83	89.2	115	21	AAB39537	Anti-IL12 antibody
40	83	89.2	115	21	AAB39539	Anti-IL12 antibody
41	83	89.2	115	21	AAB39541	Anti-IL12 antibody
42	83	89.2	115	21	AAB39543	Anti-IL12 antibody
43	83	89.2	115	21	AAB39545	Anti-IL12 antibody
44	83	89.2	115	21	AAB39547	Anti-IL12 antibody
45	83	89.2	115	21	AAB39549	Anti-IL12 antibody

ALIGNMENTS

RESULT 1
AAB67491
ID AAB67491 standard; peptide; 17 AA.
XX
AC AAB67491;
XX
DT 29-MAY-2001 (first entry)
XX
DE Human heavy chain complementarity determining region 2 (CDR2).
XX
KW Complementarity determining region; CDR; immune response; antibody;
KW cytotoxic T lymphocyte associated antigen-4; CTLA-4; B7 ligand; cancer;
KW autoimmune disease; infectious disease; inflammation; allergy;
KW rheumatoid arthritis; myasthenia gravis; lupus erythematosus;
KW multiple sclerosis; insulin-dependent diabetes mellitus; inflammation;
KW transplant rejection; graft versus host disease.
XX
OS Homo sapiens.
XX
PN WO200114424-A2.
XX
PD 01-MAR-2001.
XX
PF 24-AUG-2000; 2000WO-US23356.
XX
PR 24-AUG-1999; 99US-0150452.
XX
PA (MEDA-) MEDAREX INC.
XX
PI Korman AJ, Halk EL, Lonberg N;
XX
DR WPI; 2001-202933/20.
XX

```
PT   Novel human sequence antibody that binds to human cytotoxic T
PT   lymphocyte associated antigen-4, useful for inducing, augmenting or
PT   prolonging immune response to antigen or for suppressing immune
PT   response in patient -
XX
PS   Claim 30; Page 99; 127pp; English.
XX
CC   AAB67490-99 and AAB67501-06 represents complementarity determining
CC   regions (CDRs) of human antibodies. The antibodies specifically bind to
CC   human cytotoxic T lymphocyte associated antigen-4 (CTLA-4). Such
CC   antibodies are used in methods for inducing, augmenting or prolonging
CC   an immune response to an antigen in a patient, where the antibodies
CC   block binding of human CTLA-4 to human B7 ligands. The antibodies are
CC   also useful for treating autoimmune disease in a subject caused or
CC   exacerbated by increased activity of T cells and for treating prostate
CC   cancer, melanoma or epithelial cancer. A polyvalent or polyclonal
CC   antibody preparation comprising two antibodies of the invention are
CC   useful for suppressing a immune response in a patient. They are used for
CC   treating cancer, infectious diseases and promoting beneficial autoimmune
CC   reactions for the treatment of diseases with inflammatory or allergic
CC   components. The polyvalent or polyclonal preparations are useful for
CC   treating autoimmune diseases such as rheumatoid arthritis, myasthenia
CC   gravis and lupus erythematosus, multiple sclerosis, insulin-dependent
CC   diabetes mellitus, transplant rejection, and inflammation, graft versus
CC   host disease.
XX
SQ   Sequence   17 AA;

  Query Match             100.0%;  Score 93;  DB 22;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 4.8e-08;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 FISYDGNNKYYADSVKG 17
           |||||||||||||||||
Db       1 FISYDGNNKYYADSVKG 17


RESULT 2
AAB67508
ID   AAB67508 standard; peptide; 118 AA.
XX
AC   AAB67508;
XX
DT   29-MAY-2001  (first entry)
XX
DE   Light chain variable region of anti-CTLA-4 antibody 10D1.
XX
KW   Complementarity determining region; CDR; immune response; antibody;
KW   cytotoxic T lymphocyte associated antigen-4; CTLA-4; B7 ligand; cancer;
KW   autoimmune disease; infectious disease; inflammation; allergy;
KW   rheumatoid arthritis; myasthenia gravis; lupus erythematosus;
KW   multiple sclerosis; insulin-dependent diabetes mellitus; inflammation;
KW   transplant rejection; graft versus host disease.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Region          31..35
FT                   /note= "CDR1"
FT   Region          50..66
FT                   /note= "CDR2"
FT   Region          99..107
FT                   /note= "CDR3"
XX
PN   WO200114424-A2.
XX
PD   01-MAR-2001.
XX
PF   24-AUG-2000; 2000WO-US23356.
XX
PR   24-AUG-1999;   99US-0150452.
XX
PA   (MEDA-) MEDAREX INC.
XX
PI   Korman AJ,  Halk EL,  Lonberg N;
XX
DR   WPI; 2001-202933/20.
XX
PT   Novel human sequence antibody that binds to human cytotoxic T
PT   lymphocyte associated antigen-4, useful for inducing, augmenting or
PT   prolonging immune response to antigen or for suppressing immune
PT   response in patient -
XX
PS   Claim 25; Fig 7; 127pp; English.
XX
CC   The present sequence represents the light chain variable region of
CC   human antibody 10D1. This antibody specifically binds to human
CC   cytotoxic T lymphocyte associated antigen-4 (CTLA-4). Such antibodies
CC   are used in methods for inducing, augmenting or prolonging an immune
CC   response to an antigen in a patient, where the antibodies block
CC   binding of human CTLA-4 to human B7 ligands. The antibodies are
CC   also useful for treating autoimmune disease in a subject caused or
CC   exacerbated by increased activity of T cells and for treating prostate
CC   cancer, melanoma or epithelial cancer. A polyvalent or polyclonal
CC   antibody preparation comprising two antibodies of the invention are
CC   useful for suppressing a immune response in a patient. They are used for
CC   treating cancer, infectious diseases and promoting beneficial autoimmune
CC   reactions for the treatment of diseases with inflammatory or allergic
CC   components. The polyvalent or polyclonal preparations are useful for
CC   treating autoimmune diseases such as rheumatoid arthritis, myasthenia
CC   gravis and lupus erythematosus, multiple sclerosis, insulin-dependent
CC   diabetes mellitus, transplant rejection, and inflammation, graft versus
CC   host disease.
XX
SQ   Sequence   118 AA;

  Query Match             100.0%;  Score 93;  DB 22;  Length 118;
  Best Local Similarity   100.0%;  Pred. No. 4.3e-07;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 FISYDGNNKYYADSVKG 17
           |||||||||||||||||
Db      50 FISYDGNNKYYADSVKG 66


RESULT 3
AAB67513
ID   AAB67513 standard; peptide; 118 AA.
XX
AC   AAB67513;
XX
DT   29-MAY-2001  (first entry)
XX
DE   Heavy chain variable region of anti-CTLA-4 antibody 10D1.
XX
KW   Complementarity determining region; CDR; immune response; antibody;
KW   cytotoxic T lymphocyte associated antigen-4; CTLA-4; B7 ligand; cancer;
KW   autoimmune disease; infectious disease; inflammation; allergy;
KW   rheumatoid arthritis; myasthenia gravis; lupus erythematosus;
KW   multiple sclerosis; insulin-dependent diabetes mellitus; inflammation;
KW   transplant rejection; graft versus host disease.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Region          31..35
FT                   /note= "CDR1"
FT   Region          50..66
FT                   /note= "CDR2"
FT   Region          99..107
FT                   /note= "CDR3"
XX
PN   WO200114424-A2.
XX
PD   01-MAR-2001.
XX
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PF 24-AUG-2000; 2000WO-US23356.
XX
PR 24-AUG-1999; 99US-0150452.
XX
PA (MEDA-) MEDAREX INC.
XX
PI Korman AJ, Halk EL, Lonberg N;
XX
DR WPI; 2001-202933/20.
XX
PT Novel human sequence antibody that binds to human cytotoxic T
PT lymphocyte associated antigen-4, useful for inducing, augmenting or
PT prolonging immune response to antigen or for suppressing immune
PT response in patient -
XX
PS Claim 25; Fig 8; 127pp; English.
XX
CC The present sequence represents the heavy chain variable region of
CC human antibody 10D1. This antibody specifically binds to human
CC cytotoxic T lymphocyte associated antigen-4 (CTLA-4). Such antibodies
CC are used in methods for inducing, augmenting or prolonging an immune
CC response to an antigen in a patient, where the antibodies block
CC binding of human CTLA-4 to human B7 ligands. The antibodies are
CC also useful for treating autoimmune disease in a subject caused or
CC exacerbated by increased activity of T cells and for treating prostate
CC cancer, melanoma or epithelial cancer. A polyvalent or polyclonal
CC antibody preparation comprising two antibodies of the invention are
CC useful for suppressing a immune response in a patient. They are used for
CC treating cancer, infectious diseases and promoting beneficial autoimmune
CC reactions for the treatment of diseases with inflammatory or allergic
CC components. The polyvalent or polyclonal preparations are useful for
CC treating autoimmune diseases such as rheumatoid arthritis, myasthenia
CC gravis and lupus erythematosus, multiple sclerosis, insulin-dependent
CC diabetes mellitus, transplant rejection, and inflammation, graft versus
CC host disease.
XX
SQ Sequence 118 AA;

Query Match 100.0%; Score 93; DB 22; Length 118;
Best Local Similarity 100.0%; Pred. No. 4.3e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FISYDGNNKYYADSVKG 17
||||||||||||||||||
Db 50 FISYDGNNKYYADSVKG 66

RESULT 4
AAJ 10
ID AB39830 standard; Peptide; 17 AA.
XX
AC AAB39830;
XX
DT 05-FEB-2001 (first entry)
XX
DE Anti-hIL12 antibody heavy chain CDR2 amino acid sequence SEQ ID 346.
XX
KW Human; neutralising antibody; interleukin-12; IL-12; antiinflammatory;
KW complementarity determining region; CDR; antirheumatic; antiarthritic;
KW antisclerotic; neuroprotective; antipsoriatic; antiasthmatic; cardiant;
KW antiparasitic; antibacterial; immunosuppressive; Crohn's disease;
KW multiple sclerosis; rheumatoid arthritis.
XX
OS Homo sapiens.
XX
PN WO200056772-A1.
XX
PD 28-SEP-2000.
XX
PF 24-MAR-2000; 2000WO-US07946.
XX
PR 25-MAR-1999; 99US-0126603.
XX
PA (BADI) BASF AG.
PA (GEMY) GENETICS INST INC.
XX
PI Salfeld JG, Roguska M, Paskind M, Banerjee S, Tracey DE, White M;
PI Kaymakcalan Z, Labkovsky B, Sakorafas P, Friedrich S, Myles A;
PI Veldman GM, Venturini A, Warne NW, Widom A, Elvin JG, Duncan AR;
PI Derbyshire EJ, Carmen S, Smith S, Holtet TL, Du Fou SL;
XX
DR WPI; 2000-638250/61.
XX
PT New human antibody specific for human interleukin-12 (IL-12) used to
PT treat disorders characterized by aberrant IL-12 expression e.g. Crohn's
PT disease and multiple sclerosis -
XX
PS Claim 33; Figure 2B; 377pp; English.
XX
CC This invention relates to a new human antibody specific for human
CC interleukin-12 (IL-12). The invention also includes antigen binding
CC portions that bind to IL-12. Sequences AAB39485-B39516 represent human
CC anti-IL-12 antibody heavy and light chain complementarity determining
CC region (CDR) amino acid sequences, and also includes variable region
CC amino acid sequences. Other variable region amino acid sequences are
CC given in AAB39517-B39560 and AAB40068-B40149. Sequences AAB39561-B39771
CC represent anti-IL-12 CDR3 related amino acid sequences, AAB39772-B40063
CC represent other CDR sequences. Light chain CDR3 consensus sequences are
CC given in AAB40064-B40067. Primers used in the identification and
CC construction of the antibodies of the invention are given in
CC AAC61062-C61071. The antibody of the invention is a neutralising
CC antibody and has antirheumatic; antiarthritic; antisclerotic;
CC antiinflammatory; neuroprotective; antipsoriatic; antiasthmatic;
CC cardiant; antiparasitic; antibacterial and immunosuppressive activity.
CC The antibodies or antigen-binding fragments are useful in the treatment
CC of disorders associated with detrimental release of human IL-12,
CC especially Crohn's disease, multiple sclerosis and rheumatoid arthritis.
CC They can also be used in the manufacture of a pharmaceutical composition
CC to treat human IL-12 disorders.
XX
SQ Sequence 17 AA;

Query Match 94.6%; Score 88; DB 21; Length 17;
Best Local Similarity 94.1%; Pred. No. 2.9e-07;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FISYDGNNKYYADSVKG 17
|||||:||||||||||
Db 1 FISYDGSNKYYADSVKG 17

RESULT 5
AAU08361
ID AAU08361 standard; peptide; 17 AA.
XX
AC AAU08361;
XX
DT 17-DEC-2001 (first entry)
XX
DE Antibody heavy chain variable region CDR2 #2.
XX
KW Antibody; heavy chain; CDR2; complementarity determining region; OPGbp;
KW osteopathic; osteoprotegrin binding protein; osteoclast formation;
KW bone resorption; loss of bone mass; bone tumour; osteoporosis;
KW bone cancer; rheumatoid arthritis; hypercalcaemia of malignancy;
KW steroid-induced osteoporosis.
XX
OS Synthetic.
XX
PN WO200162932-A1.
XX
PD 30-AUG-2001.
XX
PF 23-FEB-2001; 2001WO-US05973.
XX
PR 23-FEB-2000; 2000US-0511139.

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PR   22-FEB-2001; 2001US-0791153.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Deshpande RV,  Hitz A,  Boyle WJ,  Sullivan JK;
XX
DR   WPI; 2001-557706/62.
XX
PT   Antibodies that bind antagonistically to osteoprotegrin binding
PT   protein, useful for treating osteoporosis, metastasis of cancer to
PT   bone, rheumatoid arthritis, hypercalcaemia of malignancy and
PT   steroid-induced osteoporosis -
XX
PS   Claim 14; Page 129; 239pp; English.
XX
CC   The invention relates to an antibody or antigen binding domain (or
CC   fragment, variant or derivative), which binds to an osteoprotegrin
CC   binding protein (OPGbp) and which is an antagonistic antibody.
CC   The antibody or antigen binding domain may be administered to inhibit
CC   osteoclast formation or activation, inhibit bone resorption in a mammal,
CC   prevent or treat loss of bone mass in a mammal and to prevent or treat
CC   tumour cell growth in bone. The loss of bone mass results from
CC   osteoporosis, metastasis of cancer to bone, rheumatoid arthritis,
CC   hypercalcaemia of malignancy and steroid-induced osteoporosis. The
CC   present sequence is an antibody heavy chain variable region
CC   complementarity determining region, CDR2, which can be incorporated into
CC   an antibody/antigen binding domain of the invention.
XX
SQ   Sequence   17 AA;

  Query Match            93.5%;  Score 87;  DB 22;  Length 17;
  Best Local Similarity  100.0%;  Pred. No. 4.2e-07;
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Db       2 ISYDGNNKYYADSVKG 17


RESULT 6
AAU08384
ID   AAU08384 standard; Peptide; 220 AA.
XX
AC   AAU08384;
XX
DT   17-DEC-2001  (first entry)
XX
DE   Anti-OPGbp antibody heavy chain P.
XX
KW   Antibody; OPGbp; human; P heavy chain; osteopathic;
KW   osteoprotegrin binding protein; osteoclast formation; bone resorption;
KW   loss of bone mass; bone tumour; osteoporosis; bone cancer;
KW   rheumatoid arthritis; hypercalcaemia of malignancy;
KW   steroid-induced osteoporosis; mutant; mutein.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Region          2..117
FT                   /note= "This region is specifically claimed in
FT                   claim 20"
FT   Region          2..31
FT                   /label= FR1
FT                   /note= "Framework region"
FT   Misc-difference 2
FT                   /note= "Wild-type Gln substituted by Glu"
FT   Misc-difference 7
FT                   /note= "Wild-type Glu substituted by Gln"
FT   Misc-difference 12
FT                   /note= "Wild-type Val substituted by Leu"
FT   Misc-difference 17
FT                   /note= "Wild-type Arg substituted by Gly"
FT   Misc-difference 24..25
FT                   /note= "Wild-type Ala-Ala substituted by Leu-Val"
FT   Misc-difference 31..32
FT                   /note= "Wild-type Ser-Ser substituted by Asn-Asn"
FT   Region          27..33
FT                   /label= H1
FT   Region          32..36
FT                   /label= CDR1
FT                   /note= "Complementarity determining region"
FT   Misc-difference 34
FT                   /note= "Wild-type Gly substituted by Pro"
FT   Region          37..50
FT                   /label= FR2
FT                   /note= "Framework region"
FT   Region          51..67
FT                   /label= CDR2
FT                   /note= "Complementarity determining region"
FT   Region          53..58
FT                   /label= H2
FT   Misc-difference 57
FT                   /note= "Wild-type Ser substituted by Asn"
FT   Region          68..100
FT                   /label= FR3
FT                   /note= "Framework region"
FT   Misc-difference 89
FT                   /note= "Wild-type Ala substituted by Ser"
FT   Misc-difference 99..103
FT                   /note= "Wild-type Lys-Tyr substituted by
FT                   Arg-Gly-Gly-Gly-Gly"
FT   Region          100..105
FT                   /label= H3
FT   Region          101..106
FT                   /label= CDR3
FT                   /note= "Complementarity determining region"
XX
PN   WO200162932-A1.
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PD   30-AUG-2001.
XX
PF   23-FEB-2001; 2001WO-US05973.
XX
PR   23-FEB-2000; 2000US-0511139.
PR   22-FEB-2001; 2001US-0791153.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Deshpande RV,  Hitz A,  Boyle WJ,  Sullivan JK;
XX
DR   WPI; 2001-557706/62.
DR   N-PSDB; AAS13367.
XX
PT   Antibodies that bind antagonistically to osteoprotegrin binding
PT   protein, useful for treating osteoporosis, metastasis of cancer to
PT   bone, rheumatoid arthritis, hypercalcaemia of malignancy and
PT   steroid-induced osteoporosis -
XX
PS   Example 6; Fig 11; 239pp; English.
XX
CC   The invention relates to an antibody or antigen binding domain (or
CC   fragment, variant or derivative), which binds to an osteoprotegrin
CC   binding protein (OPGbp) and which is an antagonistic antibody.
CC   The antibody or antigen binding domain may be administered to inhibit
CC   osteoclast formation or activation, inhibit bone resorption in a mammal,
CC   prevent or treat loss of bone mass in a mammal and to prevent or treat
CC   tumour cell growth in bone. The loss of bone mass results from
CC   osteoporosis, metastasis of cancer to bone, rheumatoid arthritis,
CC   hypercalcaemia of malignancy and steroid-induced osteoporosis. The
CC   present sequence is a full length, cloned anti-OPGbp antibody heavy
CC   chain P.
XX
SQ   Sequence   220 AA;

  Query Match            93.5%;  Score 87;  DB 22;  Length 220;
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GenCore version 5.1.4_p5_4578

OM protein - protein search, using sw model

Run on: April 16, 2003, 17:21:54 ; Search time 5.01053 Seconds
(without alignments)
256.547 Million cell updates/sec

Title: US-09-644-668A-32
Perfect score: 93
Sequence: 1 FISYDGNNKYYADSVKG 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 288829 seqs, 75613885 residues

To number of hits satisfying chosen parameters: 288829

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
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4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
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13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	83	89.2	249	9	US-09-880-748-1956	Sequence 1956, Ap
2	83	89.2	251	9	US-09-880-748-952	Sequence 952, App
3	83	89.2	251	9	US-09-880-748-982	Sequence 982, App
4	82	88.2	83	9	US-10-078-958-7	Sequence 7, Appli
5	82	88.2	98	9	US-10-194-975-23	Sequence 23, Appl
6	82	88.2	98	9	US-10-194-975-24	Sequence 24, Appl
7	82	88.2	98	9	US-10-194-975-25	Sequence 25, Appl
8	82	88.2	122	9	US-09-144-886-68	Sequence 68, Appl
9	82	88.2	122	9	US-09-144-886-69	Sequence 69, Appl
10	82	88.2	128	10	US-09-850-165-104	Sequence 104, App
11	82	88.2	238	9	US-09-880-748-1931	Sequence 1931, Ap
12	82	88.2	241	9	US-09-880-748-2055	Sequence 2055, Ap
13	82	88.2	247	9	US-09-880-748-924	Sequence 924, App
14	82	88.2	247	9	US-09-880-748-1330	Sequence 1330, Ap
15	82	88.2	248	9	US-09-880-748-1421	Sequence 1421, Ap
16	82	88.2	249	9	US-09-880-748-5	Sequence 5, Appli
17	82	88.2	249	9	US-09-880-748-397	Sequence 397, App
18	82	88.2	249	9	US-09-880-748-512	Sequence 512, App
19	82	88.2	249	9	US-09-880-748-892	Sequence 892, App
20	82	88.2	249	9	US-09-880-748-911	Sequence 911, App
21	82	88.2	249	9	US-09-880-748-1102	Sequence 1102, Ap
22	82	88.2	249	9	US-09-880-748-1105	Sequence 1105, Ap
23	82	88.2	249	9	US-09-880-748-1108	Sequence 1108, Ap
24	82	88.2	249	9	US-09-880-748-1110	Sequence 1110, Ap
25	82	88.2	249	9	US-09-880-748-1111	Sequence 1111, Ap
26	82	88.2	249	9	US-09-880-748-1113	Sequence 1113, Ap
27	82	88.2	249	9	US-09-880-748-1115	Sequence 1115, Ap
28	82	88.2	249	9	US-09-880-748-1117	Sequence 1117, Ap
29	82	88.2	249	9	US-09-880-748-1119	Sequence 1119, Ap
30	82	88.2	249	9	US-09-880-748-1724	Sequence 1724, Ap
31	82	88.2	249	9	US-09-880-748-1725	Sequence 1725, Ap
32	82	88.2	252	9	US-09-880-748-1201	Sequence 1201, Ap
33	82	88.2	252	9	US-09-880-748-1394	Sequence 1394, Ap
34	82	88.2	252	9	US-09-880-748-1519	Sequence 1519, Ap
35	82	88.2	252	9	US-09-880-748-1627	Sequence 1627, Ap
36	82	88.2	252	9	US-09-880-748-1731	Sequence 1731, Ap
37	82	88.2	254	9	US-09-880-748-977	Sequence 977, App
38	82	88.2	254	9	US-09-880-748-981	Sequence 981, App
39	82	88.2	254	9	US-09-880-748-983	Sequence 983, App
40	82	88.2	256	9	US-09-880-748-839	Sequence 839, App
41	81	87.1	17	10	US-09-828-708-24	Sequence 24, Appl
42	81	87.1	101	10	US-09-828-708-10	Sequence 10, Appl
43	81	87.1	241	9	US-09-880-748-1887	Sequence 1887, Ap
44	81	87.1	241	9	US-09-880-748-1901	Sequence 1901, Ap
45	81	87.1	243	9	US-09-880-748-1935	Sequence 1935, Ap

ALIGNMENTS

RESULT 1
US-09-880-748-1956
; Sequence 1956, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1956
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1956

Query Match 89.2%; Score 83; DB 9; Length 249;
Best Local Similarity 88.2%; Pred. No. 5.9e-05;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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Db      50 FISYDGSHKYYADSVKG 66
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RESULT 2
US-09-880-748-952
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; Publication No. US20030059937A1
; GENERAL INFORMATION:

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;  APPLICANT: Ruben et al.
;  TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
;  FILE REFERENCE: PF523
;  CURRENT APPLICATION NUMBER: US/09/880,748
;  CURRENT FILING DATE:  2001-06-15
;  PRIOR APPLICATION NUMBER: 60/212,210
;  PRIOR FILING DATE: 2000-06-15
;  PRIOR APPLICATION NUMBER: 60/240,816
;  PRIOR FILING DATE: 2000-10-17
;  PRIOR APPLICATION NUMBER: 60/276,248
;  PRIOR FILING DATE: 2001-03-16
;  PRIOR APPLICATION NUMBER: 60/277,379
;  PRIOR FILING DATE: 2001-03-21
;  PRIOR APPLICATION NUMBER: 60/293,499
;  PRIOR FILING DATE: 2001-05-25
;  NUMBER OF SEQ ID NOS: 3239
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 952
;    LENGTH: 251
;    TYPE: PRT
;    ORGANISM: Homo sapiens
US-09-880-748-952

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  Matches   15;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 FISYDGNNKYYADSVKG 17
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Db      50 FIRYDGSNKYYADSVKG 66


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; Publication No. US20030059937A1
; GENERAL INFORMATION:
;  APPLICANT: Ruben et al.
;  TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
;  FILE REFERENCE: PF523
;  CURRENT APPLICATION NUMBER: US/09/880,748
;  CURRENT FILING DATE:  2001-06-15
;  PRIOR APPLICATION NUMBER: 60/212,210
;  PRIOR FILING DATE: 2000-06-15
;  PRIOR APPLICATION NUMBER: 60/240,816
;  PRIOR FILING DATE: 2000-10-17
;  PRIOR APPLICATION NUMBER: 60/276,248
;  PRIOR FILING DATE: 2001-03-16
;  PRIOR APPLICATION NUMBER: 60/277,379
;  PRIOR FILING DATE: 2001-03-21
;  PRIOR APPLICATION NUMBER: 60/293,499
;  PRIOR FILING DATE: 2001-05-25
;  NUMBER OF SEQ ID NOS: 3239
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 982
;    LENGTH: 251
;    TYPE: PRT
;    ORGANISM: Homo sapiens
US-09-880-748-982

  Query Match             89.2%;  Score 83;  DB 9;  Length 251;
  Best Local Similarity   88.2%;  Pred. No. 5.9e-05;
  Matches   15;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 FISYDGNNKYYADSVKG 17
           || |||:||||||||||
Db      50 FIRYDGSNKYYADSVKG 66


RESULT 4
US-10-078-958-7
; Sequence 7, Application US/10078958
; Publication No. US20030070185A1
; GENERAL INFORMATION:
;  APPLICANT: JAKOBOVITS, AYA
;  APPLICANT:  KUCHERLAPATI, RAJU
;  APPLICANT:  KLAPHOLZ, SUSAN
;  APPLICANT:  MENDEZ, MICHAEL J.
;  APPLICANT:  GREEN, LARRY
;  TITLE OF INVENTION: TRANSGENIC MAMMALS HAVING HUMAN Ig LOCI INCLUDING
;  TITLE OF INVENTION:  PLURAL Vh AND Vk REGIONS AND ANTIBODIES PRODUCED
;  TITLE OF INVENTION:  THEREFROM
;  FILE REFERENCE: CELL 4.18 CON
;  CURRENT APPLICATION NUMBER: US/10/078,958
;  CURRENT FILING DATE:  2002-02-19
;  PRIOR APPLICATION NUMBER: 08/759,620
;  PRIOR FILING DATE: 1996-12-03
;  NUMBER OF SEQ ID NOS: 79
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
;    LENGTH: 83
;    TYPE: PRT
;    ORGANISM: Homo sapiens
;    FEATURE:
;    NAME/KEY: MOD_RES
;    LOCATION: (22)
;    OTHER INFORMATION: Variable amino acid
US-10-078-958-7

  Query Match             88.2%;  Score 82;  DB 9;  Length 83;
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  Matches   15;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 ISYDGNNKYYADSVKG 17
           |||||:||||||||||
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RESULT 5
US-10-194-975-23
; Sequence 23, Application US/10194975
; Publication No. US20030039649A1
; GENERAL INFORMATION:
;  APPLICANT: Foote, Jefferson
;  TITLE OF INVENTION: Super Humanized Antibodies
;  FILE REFERENCE: 501231.01
;  CURRENT APPLICATION NUMBER: US/10/194,975
;  CURRENT FILING DATE:  2002-10-10
;  PRIOR APPLICATION NUMBER: US 60/305,111
;  PRIOR FILING DATE: 2001-07-12
;  NUMBER OF SEQ ID NOS: 122
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
;    LENGTH: 98
;    TYPE: PRT
;    ORGANISM: Homo sapiens
US-10-194-975-23

  Query Match             88.2%;  Score 82;  DB 9;  Length 98;
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  Matches   15;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 ISYDGNNKYYADSVKG 17
           |||||:||||||||||
Db      51 ISYDGSNKYYADSVKG 66


RESULT 6
US-10-194-975-24
; Sequence 24, Application US/10194975
; Publication No. US20030039649A1
; GENERAL INFORMATION:
;  APPLICANT: Foote, Jefferson
;  TITLE OF INVENTION: Super Humanized Antibodies
;  FILE REFERENCE: 501231.01
;  CURRENT APPLICATION NUMBER: US/10/194,975
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GenCore version 5.1.4_p5_4578

OM protein - protein search, using sw model

Run on: April 16, 2003, 17:15:40 ; Search time 4.35439 Seconds
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114.870 Million cell updates/sec

Title: US-09-644-668A-32
Perfect score: 93
Sequence: 1 FISYDGNNKYYADSVKG 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

To number of hits satisfying chosen parameters: 262574

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	82	88.2	98	1	US-08-211-202-118	Sequence 118, App
2	82	88.2	116	1	US-08-211-202-141	Sequence 141, App
	82	88.2	117	3	US-08-545-809A-115	Sequence 115, App
	82	88.2	119	1	US-08-331-398A-46	Sequence 46, Appl
5	82	88.2	119	2	US-08-331-397B-46	Sequence 46, Appl
6	82	88.2	119	2	US-08-759-804A-46	Sequence 46, Appl
7	82	88.2	119	4	US-09-227-693-46	Sequence 46, Appl
8	82	88.2	120	1	US-08-211-202-135	Sequence 135, App
9	82	88.2	120	1	US-07-942-245-35	Sequence 35, Appl
10	82	88.2	123	4	US-08-983-607-38	Sequence 38, Appl
11	82	88.2	128	1	US-08-478-039-96	Sequence 96, Appl
12	82	88.2	128	1	US-08-476-349A-96	Sequence 96, Appl
13	77	82.8	124	4	US-09-240-274-5	Sequence 5, Appli
14	77	82.8	124	4	US-09-240-274-6	Sequence 6, Appli
15	77	82.8	125	1	US-08-276-852-72	Sequence 72, Appl
16	77	82.8	125	1	US-08-276-852-73	Sequence 73, Appl
17	77	82.8	125	1	US-08-276-852-74	Sequence 74, Appl
18	77	82.8	125	1	US-08-276-852-75	Sequence 75, Appl
19	77	82.8	125	1	US-08-276-852-76	Sequence 76, Appl
20	77	82.8	125	1	US-08-276-852-77	Sequence 77, Appl
21	77	82.8	125	1	US-08-899-575-72	Sequence 72, Appl
22	77	82.8	125	1	US-08-899-575-73	Sequence 73, Appl
23	77	82.8	125	1	US-08-899-575-74	Sequence 74, Appl
24	77	82.8	125	1	US-08-899-575-75	Sequence 75, Appl
25	77	82.8	125	1	US-08-899-575-76	Sequence 76, Appl
26	77	82.8	125	1	US-08-899-575-77	Sequence 77, Appl
27	77	82.8	125	1	US-08-899-575-72	Sequence 72, Appl
28	77	82.8	125	1	US-08-899-575-73	Sequence 73, Appl
29	77	82.8	125	1	US-08-899-575-74	Sequence 74, Appl
30	77	82.8	125	1	US-08-899-575-75	Sequence 75, Appl
31	77	82.8	125	1	US-08-899-575-76	Sequence 76, Appl
32	77	82.8	125	1	US-08-899-575-77	Sequence 77, Appl
33	77	82.8	125	5	PCT-US95-08743-72	Sequence 72, Appl
34	77	82.8	125	5	PCT-US95-08743-73	Sequence 73, Appl
35	77	82.8	125	5	PCT-US95-08743-74	Sequence 74, Appl
36	77	82.8	125	5	PCT-US95-08743-75	Sequence 75, Appl
37	77	82.8	125	5	PCT-US95-08743-76	Sequence 76, Appl
38	77	82.8	125	5	PCT-US95-08743-77	Sequence 77, Appl
39	77	82.8	126	4	US-09-240-274-16	Sequence 16, Appl
40	77	82.8	126	4	US-09-240-274-152	Sequence 152, App
41	77	82.8	127	4	US-09-240-274-139	Sequence 139, App
42	77	82.8	141	1	US-08-259-372A-2	Sequence 2, Appli
43	77	82.8	141	1	US-08-468-671-2	Sequence 2, Appli
44	76	81.7	179	4	US-08-862-124-2	Sequence 2, Appli
45	76	81.7	287	4	US-08-862-124-17	Sequence 17, Appl

ALIGNMENTS

```
RESULT 1
US-08-211-202-118
; Sequence 118, Application US/08211202
; Patent No. 5565332
;  GENERAL INFORMATION:
;    APPLICANT:  HOOGENBOOM, Hendricus Renerus Jacobus Matteus
;    APPLICANT:  BAIER, Michael
;    APPLICANT:  JESPERS, Laurent Stephane Anne Therese
;    APPLICANT:  WINTER, Gregory Paul
;    TITLE OF INVENTION:  Production of  chimeric antibodies - a
;    TITLE OF INVENTION:  combinatorial approach
;    NUMBER OF SEQUENCES:  144
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  David W. Clough, Marshall O'Toole Gerstein Murray &
;      ADDRESSEE:  Borun
;      STREET:  6300 Sears Tower, 233 South Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60606-6402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25 (EPO)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/211,202
;      FILING DATE:  23-SEP-1992
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9120252.3
;      FILING DATE:  23-SEP-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9120377.8
;      FILING DATE:  25-SEP-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9206318.9
;      FILING DATE:  24-MAR-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9206372.6
;      FILING DATE:  24-MAR-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/GB92/00883
;      FILING DATE:  15-MAY-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  David W. Clough
;      REGISTRATION NUMBER:  36,107
;      REFERENCE/DOCKET NUMBER:  28111/31960
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312-474-6300
```

```
;      TELEFAX:  312-474-0448
;      TELEX:  25-3856
;   INFORMATION FOR SEQ ID NO:  118:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  98 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-08-211-202-118

  Query Match             88.2%;  Score 82;  DB 1;  Length 98;
  Best Local Similarity   93.8%;  Pred. No. 4.7e-06;
  Matches   15;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 ISYDGNNKYYADSVKG 17
           |||||:||||||||||
Db      51 ISYDGSNKYYADSVKG 66


RE   2
US     211-202-141
; Sequence 141, Application US/08211202
; Patent No. 5565332
;  GENERAL INFORMATION:
;     APPLICANT:  HOOGENBOOM, Hendricus Renerus Jacobus Matteus
;     APPLICANT:  BAIER, Michael
;     APPLICANT:  JESPERS, Laurent Stephane Anne Therese
;     APPLICANT:  WINTER, Gregory Paul
;     TITLE OF INVENTION:  Production of  chimeric antibodies - a
;     TITLE OF INVENTION:  combinatorial approach
;     NUMBER OF SEQUENCES:  144
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  David W. Clough, Marshall O'Toole Gerstein Murray &
;       ADDRESSEE:  Borun
;       STREET:  6300 Sears Tower, 233 South Wacker Drive
;       CITY:  Chicago
;       STATE:  Illinois
;       COUNTRY:  USA
;       ZIP:  60606-6402
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25 (EPO)
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/211,202
;       FILING DATE:  23-SEP-1992
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  GB 9120252.3
;       FILING DATE:  23-SEP-1991
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  GB 9120377.8
;       FILING DATE:  25-SEP-1991
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  GB 9206318.9
;       FILING DATE:  24-MAR-1992
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  GB 9206372.6
;       FILING DATE:  24-MAR-1992
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  PCT/GB92/00883
;       FILING DATE:  15-MAY-1992
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  David W. Clough
;       REGISTRATION NUMBER:  36,107
;       REFERENCE/DOCKET NUMBER:  28111/31960
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  312-474-6300
;       TELEFAX:  312-474-0448
;       TELEX:  25-3856
;   INFORMATION FOR SEQ ID NO:  141:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  116 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-08-211-202-141

  Query Match             88.2%;  Score 82;  DB 1;  Length 116;
  Best Local Similarity   93.8%;  Pred. No. 5.6e-06;
  Matches   15;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 ISYDGNNKYYADSVKG 17
           |||||:||||||||||
Db      51 ISYDGSNKYYADSVKG 66


RESULT 3
US-08-545-809A-115
; Sequence 115, Application US/08545809A
; Patent No. 6096878
;  GENERAL INFORMATION:
;     APPLICANT:  Honjo, Tasuku
;     APPLICANT:  Matsuda, Fumihiko
;     TITLE OF INVENTION:  HUMAN IMMUNOGLOBULIN VH GENE
;     TITLE OF INVENTION:  SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
;     NUMBER OF SEQUENCES:  145
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Fish & Richardson, P.C.
;       STREET:  225 Franklin Street
;       CITY:  Boston
;       STATE:  MA
;       COUNTRY:  US
;       ZIP:  02110-2804
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Diskette
;       COMPUTER:  IBM Compatible
;       OPERATING SYSTEM:  Windows95
;       SOFTWARE:  FastSEQ for Windows Version 2.0
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/545,809A
;       FILING DATE:  27-MAR-1996
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  PCT/JP93/00603
;       FILING DATE:  10-MAY-1993
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Freeman, John W.
;       REGISTRATION NUMBER:  29,066
;       REFERENCE/DOCKET NUMBER:  06501/004001
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  617-542-5070
;       TELEFAX:  617-542-8906
;       TELEX:  200154
;   INFORMATION FOR SEQ ID NO:  115:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  117 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-08-545-809A-115

  Query Match             88.2%;  Score 82;  DB 3;  Length 117;
  Best Local Similarity   93.8%;  Pred. No. 5.7e-06;
  Matches   15;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 ISYDGNNKYYADSVKG 17
           |||||:||||||||||
Db      70 ISYDGSNKYYADSVKG 85


RESULT 4
US-08-331-398A-46
; Sequence 46, Application US/08331398A
; Patent No. 5608039
;  GENERAL INFORMATION:
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GenCore version 5.1.4_p5_4578

OM protein - protein search, using sw model

Run on: April 16, 2003, 17:11:36 ; Search time 2.77895 Seconds
(without alignments)
311.344 Million cell updates/sec

Title: US-09-644-668A-35
Perfect score: 54
Sequence: 1 QQYGSSPWT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	54	100.0	108	2	C30608	Ig kappa chain V-I
2	54	100.0	129	1	K3HUHI	Ig kappa chain pre
3	51	94.4	118	2	T03036	Ig light chain - h
	45	83.3	91	2	S67940	Ig kappa chain V r
	45	83.3	92	2	S37513	Ig kappa chain V r
6	45	83.3	109	2	A30608	Ig kappa chain V-I
7	45	83.3	109	2	H30601	Ig kappa chain V-I
8	44	81.5	92	2	S37524	Ig kappa chain V r
9	44	81.5	108	1	K3HUB6	Ig kappa chain V-I
10	44	81.5	109	2	G30607	Ig kappa chain V-I
11	43.5	80.6	93	2	S37526	Ig kappa chain V r
12	43	79.6	88	2	PL0261	Ig kappa chain V r
13	43	79.6	106	2	PL0260	Ig kappa chain V r
14	43	79.6	130	1	KVMSM4	Ig kappa chain pre
15	42	77.8	92	2	S37533	Ig kappa chain V r
16	42	77.8	96	2	G38601	Ig kappa chain V r
17	42	77.8	125	2	S40333	Ig kappa chain V-J
18	42	77.8	136	2	A49137	Ig kappa chain pre
19	41	75.9	92	2	S37510	Ig kappa chain V r
20	41	75.9	102	2	A34153	Ig kappa chain V-I
21	41	75.9	108	2	B30608	Ig kappa chain V-I
22	41	75.9	109	1	K3HUSI	Ig kappa chain V-I
23	41	75.9	109	2	B30601	Ig kappa chain V-I
24	41	75.9	109	2	C30601	Ig kappa chain V-I
25	41	75.9	129	2	S49532	anti-Sm antibody V
26	41	75.9	215	2	A23746	Ig kappa chain V-I
27	41	75.9	391	2	T40029	hypothetical prote
28	40	74.1	92	2	S37519	Ig kappa chain V r
29	40	74.1	92	2	S37517	Ig kappa chain V r
30	40	74.1	97	2	PH1085	Ig light chain V r
31	40	74.1	100	2	S29590	Ig kappa chain V r
32	40	74.1	106	2	PL0259	Ig kappa chain V r
33	40	74.1	109	1	K3HUTI	Ig kappa chain V-I
34	40	74.1	109	2	G30601	Ig kappa chain V-I
35	40	74.1	109	2	D30601	Ig kappa chain V-I
36	40	74.1	109	2	F44151	Ig kappa chain V r
37	40	74.1	109	2	S47181	Ig kappa chain - h
38	40	74.1	121	2	S40327	Ig kappa chain - h
39	40	74.1	127	2	S04577	Ig kappa chain pre
40	40	74.1	215	2	H85580	hypothetical prote
41	40	74.1	261	1	QBBPL	recombination prot
42	40	74.1	261	2	G90775	recombination prot
43	40	74.1	261	2	A98004	recombination prot
44	40	74.1	261	2	E85848	hypothetical prote
45	40	74.1	261	2	H85637	recombination prot

ALIGNMENTS

RESULT 1
C30608
Ig kappa chain V-III region (Pie) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 21-Jan-2000
C;Accession: C30608
R;Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Solc
J. Immunol. 142, 3158-3163, 1989
A;Title: Structural and idiotypic characterization of the L chains of human IgM autoanti
A;Reference number: A30601; MUID:89215279; PMID:2496160
A;Accession: C30608
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-108 <GON>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-91/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 54; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       1 QQYGSSPWT 9
           |||||||||
Db      90 QQYGSSPWT 98
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RESULT 2
K3HUHI
Ig kappa chain precursor V-III region (Hic) - human
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 21-Jan-2000
C;Accession: PL0021
R;Kipps, T.J.; Tomhave, E.; Chen, P.P.; Carson, D.A.
J. Exp. Med. 167, 840-852, 1988
A;Title: Autoantibody-associated kappa light chain variable region gene expressed in chr
A;Reference number: PL0021; MUID:88171307; PMID:3127527
A;Accession: PL0021
A;Molecule type: mRNA
A;Residues: 1-129 <KIP>
C;Comment: The protein is one of the surface immunoglobulin M autoantibodies expressed i
C;Genetics:
A;Gene: GDB:IGKV3
A;Cross-references: GDB:136266
A;Map position: 2p12-2p11
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: autoantibody; chronic lymphocytic leukemia; heterotetramer; immunoglobulin
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-129/Product: Ig kappa chain V-III region (Hic) #status predicted <MAT>
F;21-117/Region: V segment

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F;36-111/Domain: immunoglobulin homology <IMM>
F;44-55/Region: complementarity-determining 1
F;71-77/Region: complementarity-determining 2
F;110-117/Region: complementarity-determining 3
F;118-129/Region: J segment (JK1)
F;43-109/Disulfide bonds: #status predicted

  Query Match             100.0%;  Score 54;  DB 1;  Length 129;
  Best Local Similarity   100.0%;  Pred. No. 0.024;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 QQYGSSPWT 9
           |||||||||
Db     110 QQYGSSPWT 118


RESULT 3
T03036
Ig light chain - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 21-Jul-2000
C;Accession: T03036
R;van Es, J.H.; Gmelig Meyling, F.H.J.; van de Akker, W.R.M.; Aanstoot, H.; Derksen, R.H
J. Exp. Med. 173, 461-470, 1991
A;Title: Somatic mutations in the variable regions of a human IgG anti-double-stranded D
A;Reference number: JH0428; MUID:91108344; PMID:1899104
A;Accession: T03036
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-118 <VAN>
A;Cross-references: EMBL:X56594; NID:g36657; PIDN:CAA39932.1; PID:g1335324
A;Experimental source: B-cell
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;20-95/Domain: immunoglobulin homology <IMM>

  Query Match             94.4%;  Score 51;  DB 2;  Length 118;
  Best Local Similarity   88.9%;  Pred. No. 0.072;
  Matches    8;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 QQYGSSPWT 9
           ||||:||||
Db      94 QQYGNSPWT 102


RESULT 4
S67940
Ig kappa chain V region, subgroup III (clone MH52) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 19-Mar-1997 #sequence_revision 09-May-1997 #text_change 20-Mar-1998
C;Accession: S67940
R;Hexham, J.M.; Furmaniak, J.; Pegg, C.; Burton, D.R.; Smith, B.R.
Autoimmunity 12, 135-141, 1992
A;Title: Cloning of a human autoimmune response: preparation and sequencing of a human a
A;Reference number: S67940; MUID:92314301; PMID:1617110
A;Accession: S67940
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-91 <HEX>
A;Cross-references: EMBL:X73852
C;Superfamily: immunoglobulin V region; immunoglobulin homology

  Query Match             83.3%;  Score 45;  DB 2;  Length 91;
  Best Local Similarity   88.9%;  Pred. No. 0.61;
  Matches    8;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 QQYGSSPWT 9
           |||||||:|
Db      71 QQYGSSPYT 79


RESULT 5
S37513
Ig kappa chain V region (V-kappa 3) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: S37513
R;Klein, U.; Kueppers, R.; Rajewsky, K.
submitted to the EMBL Data Library, September 1993
A;Description: Human IgM(+)IgD(+) cells, the major B cell subset in the peripheral bl
A;Reference number: S37501
A;Accession: S37513
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-92 <KLE>
A;Cross-references: EMBL:Z26598; NID:g405668; PIDN:CAA81352.1; PID:g405669
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

  Query Match             83.3%;  Score 45;  DB 2;  Length 92;
  Best Local Similarity   88.9%;  Pred. No. 0.61;
  Matches    8;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 QQYGSSPWT 9
           |||||||:|
Db      73 QQYGSSPYT 81


RESULT 6
A30608
Ig kappa chain V-III region (Son) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 21-Jan-2000
C;Accession: A30608
R;Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Sc
J. Immunol. 142, 3158-3163, 1989
A;Title: Structural and idiotypic characterization of the L chains of human IgM autoan
A;Reference number: A30601; MUID:89215279; PMID:2496160
A;Accession: A30608
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-109 <GON>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-91/Domain: immunoglobulin homology <IMM>

  Query Match             83.3%;  Score 45;  DB 2;  Length 109;
  Best Local Similarity   88.9%;  Pred. No. 0.73;
  Matches    8;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 QQYGSSPWT 9
           |||||||:|
Db      90 QQYGSSPYT 98


RESULT 7
H30601
Ig kappa chain V-III region (Gar and Flo) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 21-Jan-2000
C;Accession: H30601; E30601
R;Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Sc
J. Immunol. 142, 3158-3163, 1989
A;Title: Structural and idiotypic characterization of the L chains of human IgM autoan
A;Reference number: A30601; MUID:89215279; PMID:2496160
A;Accession: H30601
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-109 <GON1>
A;Accession: E30601
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-109 <GON2>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-91/Domain: immunoglobulin homology <IMM>
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GenCore version 5.1.4_p5_4578

OM protein - protein search, using sw model

Run on: April 16, 2003, 16:57:42 ; Search time 1.76842 Seconds
(without alignments)
211.085 Million cell updates/sec

Title: US-09-644-668A-35
Perfect score: 54
Sequence: 1 QQYGSSPWT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

To number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	54	100.0	129	1	KV3M_HUMAN	P18136 homo sapien
2	44	81.5	108	1	KV3A_HUMAN	P01619 homo sapien
3	43	79.6	130	1	KV5G_MOUSE	P01639 mus musculu
4	41	75.9	109	1	KV3B_HUMAN	P01620 homo sapien
5	40	74.1	109	1	KV3D_HUMAN	P01622 homo sapien
6	40	74.1	261	1	VBET_LAMBD	P03698 bacteriopha
7	39	72.2	367	1	VE2_HPV11	P04015 human papil
	39	72.2	377	1	VE2_PCPV1	Q02264 pygmy chimp
	39	72.2	461	1	FUCO_DICDI	P10901 dictyosteli
10	38	70.4	109	1	KV3G_HUMAN	P04206 homo sapien
11	38	70.4	497	1	VE2_HPV20	P50766 human papil
12	37	68.5	108	1	KV1R_HUMAN	P01610 homo sapien
13	37	68.5	129	1	KV3L_HUMAN	P18135 homo sapien
14	37	68.5	377	1	VE2_HPV44	Q80916 human papil
15	37	68.5	483	1	VE2_HPV14	P36783 human papil
16	37	68.5	1066	1	HYSA_STRPN	Q54873 streptococc
17	36	66.7	128	1	KV3K_HUMAN	P06311 homo sapien
18	36	66.7	134	1	KV4C_HUMAN	P06314 homo sapien
19	36	66.7	382	1	VE2_HPV15	P36784 human papil
20	36	66.7	388	1	VE2_HPV29	P50772 human papil
21	36	66.7	396	1	VE2_HPV50	Q80930 human papil
22	36	66.7	398	1	VE2_HPV42	P27223 human papil
23	36	66.7	452	1	VE2_HPV17	P36785 human papil
24	36	66.7	461	1	VE2_HPV09	P36780 human papil
25	35	64.8	108	1	KV1B_HUMAN	P01594 homo sapien
26	35	64.8	227	1	IDI1_SCHPO	Q10132 schizosacch
27	35	64.8	378	1	VE2_HPV55	Q80937 human papil
28	35	64.8	436	1	VE2_HPV22	P50768 human papil
29	35	64.8	493	1	VE2_HPV19	P36786 human papil
30	35	64.8	2483	1	COA2_HUMAN	O00763 homo sapien
31	34.5	63.9	479	1	PAX3_HUMAN	P23760 homo sapien
32	34.5	63.9	479	1	PAX3_MOUSE	P24610 mus musculu
33	34	63.0	218	1	Y522_HAEIN	Q57256 haemophilus
34	34	63.0	254	1	HM36_CAEEL	Q93352 caenorhabdi
35	34	63.0	288	1	CYST_MARPO	P26246 marchantia
36	34	63.0	493	1	PCD_ARTOX	Q01470 arthrobacte
37	34	63.0	575	1	I10R_MOUSE	Q61727 mus musculu
38	34	63.0	582	1	ZF36_HUMAN	P16415 homo sapien
39	34	63.0	711	1	HGFL_HUMAN	P26927 homo sapien
40	34	63.0	716	1	HGFL_MOUSE	P26928 mus musculu
41	34	63.0	1396	1	VLTF_BPT5	P13390 bacteriopha
42	33	61.1	61	1	XYLU_ECOLI	P05056 escherichia
43	33	61.1	108	1	KV1V_HUMAN	P04430 homo sapien
44	33	61.1	108	1	Y388_MYCPN	P75209 mycoplasma
45	33	61.1	245	1	DMA_SQUAC	P36963 squalus aca

ALIGNMENTS

RESULT 1
KV3M_HUMAN
ID KV3M_HUMAN STANDARD; PRT; 129 AA.
AC P18136;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region HIC precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88171307; PubMed=3127527;
RA Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;
RT "Autoantibody-associated kappa light chain variable region gene
RT expressed in chronic lymphocytic leukemia with little or no somatic
RT mutation. Implications for etiology and immunotherapy.";
RL J. Exp. Med. 167:840-852(1988).
CC -!- DISEASE: THE PROTEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN M
CC AUTOANTIBODIES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCYTIC
CC LEUKEMIA.
DR PIR; PL0021; K3HUHI.
DR HSSP; P80362; 1WTL.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGv; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 129 IG KAPPA CHAIN V-III REGION HIC.
FT DOMAIN 21 43 FRAMEWORK-1.
FT DOMAIN 44 55 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 56 70 FRAMEWORK-2.
FT DOMAIN 71 77 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 78 109 FRAMEWORK-3.
FT DOMAIN 110 118 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 119 129 JK1 SEGMENT.
FT DISULFID 43 109 BY SIMILARITY.
FT NON_TER 129 129
SQ SEQUENCE 129 AA; 14070 MW; 7395528EA2BB74D6 CRC64;

Query Match 100.0%; Score 54; DB 1; Length 129;
Best Local Similarity 100.0%; Pred. No. 0.0055;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQYGSSPWT 9
||||||||| |
Db 110 QQYGSSPWT 118

RESULT 2
KV3A_HUMAN
ID KV3A_HUMAN STANDARD; PRT; 108 AA.
AC P01619;

```
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-III region B6.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RA   Milstein C.;
RT   "The basic sequences of immunoglobulin kappa chains: sequence studies
RT   of Bence Jones proteins Rad, Fr4 and B6.";
RL   FEBS Lett. 2:301-304(1969).
CC   -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR   PIR; A01891; K3HUB6.
DR   HSSP; P80362; 1WTL.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Bence-Jones protein.
FT   DISULFID     23     89       BY SIMILARITY.
FT   NON_TER     108    108
SQ   SEQUENCE   108 AA;  11635 MW;  8BC14FF07A419E3D CRC64;

  Query Match             81.5%;  Score 44;  DB 1;  Length 108;
  Best Local Similarity   88.9%;  Pred. No. 0.29;
  Matches    8;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 QQYGSSPWT 9
           |||||||:|
Db      90 QQYGSSPPT 98


RESULT 3
KV5G_MOUSE
ID   KV5G_MOUSE     STANDARD;      PRT;   130 AA.
AC   P01639; P01640;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-V region MOPC 41 precursor.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=79221900; PubMed=111146;
RA   Seidman J.G., Max E.E., Leder P.;
RT   "A kappa-immunoglobulin gene is formed by site-specific recombination
RT   without further somatic mutation.";
RL   Nature 280:370-375(1979).
RN   [2]
RP   SEQUENCE OF 1-33.
RX   MEDLINE=77148916; PubMed=403522;
RA   Burstein Y., Schechter I.;
RT   "Amino acid sequence of the NH2-terminal extra piece segments of the
RT   precursors of mouse immunoglobulin lambda1-type and kappa-type light
RT   chains.";
RL   Proc. Natl. Acad. Sci. U.S.A. 74:716-720(1977).
RN   [3]
RP   SEQUENCE OF 23-130.
RX   MEDLINE=67056897; PubMed=4162931;
RA   Gray W.R., Dreyer W.J., Hood L.;
RT   "Mechanism of antibody synthesis: size differences between mouse
RT   kappa chains.";
RL   Science 155:465-467(1967).
CC   -!- MISCELLANEOUS: THIS PRECURSOR WAS SYNTHESIZED IN A CELL-FREE
CC       SYSTEM DIRECTED BY MRNA ISOLATED FROM MYELOMA POLYSOMES.
CC   -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR   PIR; A01922; KVMSM4.
DR   HSSP; P01607; 1REI.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Signal; Bence-Jones protein.
FT   SIGNAL        1     22
FT   CHAIN        23    130       IG KAPPA CHAIN V-V REGION MOPC 41.
FT   DOMAIN       23     45       FRAMEWORK-1.
FT   DOMAIN       46     56       COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN       57     71       FRAMEWORK-2.
FT   DOMAIN       72     78       COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN       79    110       FRAMEWORK-3.
FT   DOMAIN      111    119       COMPLEMENTARITY-DETERMINING-3.
FT   DOMAIN      120    129       FRAMEWORK-4.
FT   DISULFID     45    110       BY SIMILARITY.
FT   VARIANT       1      2       MISSING (IN 25% OF THE MOLECULES).
FT   NON_TER     130    130
SQ   SEQUENCE   130 AA;  14311 MW;  5EFE0FE71D5F1BEC CRC64;

  Query Match             79.6%;  Score 43;  DB 1;  Length 130;
  Best Local Similarity   87.5%;  Pred. No. 0.53;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2 QYGSSPWT 9
           || |||||
Db     112 QYASSPWT 119


RESULT 4
KV3B_HUMAN
ID   KV3B_HUMAN     STANDARD;      PRT;   109 AA.
AC   P01620;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-III region SIE.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=82046598; PubMed=6794615;
RA   Andrews D.W., Capra J.D.;
RT   "Amino acid sequence of the variable regions of light chains from two
RT   idiotypically cross-reactive human IgM anti-gamma-globulins of the Wa
RT   group.";
RL   Biochemistry 20:5816-5822(1981).
CC   -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
CC       GLOBULIN ACTIVITY.
DR   PIR; A01892; K3HUSI.
DR   HSSP; P80362; 1WTL.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region.
FT   DISULFID     23     89       BY SIMILARITY.
FT   NON_TER     109    109
SQ   SEQUENCE   109 AA;  11775 MW;  7689C3ECD646FFB4 CRC64;

  Query Match             75.9%;  Score 41;  DB 1;  Length 109;
  Best Local Similarity   88.9%;  Pred. No. 1;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 QQYGSSPWT 9
           |||||||:|
Db      90 QQYGSSPQT 98


RESULT 5
KV3D_HUMAN
```

GenCore version 5.1.4_p5_4578

OM protein - protein search, using sw model

Run on: April 16, 2003, 17:13:59 ; Search time 9.22105 Seconds
(without alignments)
201.108 Million cell updates/sec

Title: US-09-644-668A-35
Perfect score: 54
Sequence: 1 QQYGSSPWT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Tot number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_21:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

'red. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	41	75.9	109	4	Q9UL78	Q9ul78 homo sapien
2	41	75.9	141	16	Q99Y45	Q99y45 streptococc
3	41	75.9	373	3	O13664	O13664 schizosacch
4	41	75.9	391	3	O42996	O42996 schizosacch
5	41	75.9	414	12	Q9J028	Q9j028 rabbit oral
6	41	75.9	444	12	O56955	O56955 human papil
7	40	74.1	215	16	Q8X3X3	Q8x3x3 escherichia
8	40	74.1	261	2	Q9LA41	Q9la41 shigella dy
9	40	74.1	261	9	Q9T1N6	Q9t1n6 bacteriopha
10	40	74.1	261	9	Q9XJH9	Q9xjh9 bacteriopha
11	40	74.1	261	16	Q8Z7Y3	Q8z7y3 salmonella
12	40	74.1	261	16	Q9EYA5	Q9eya5 escherichia
13	40	74.1	261	16	Q9KXG2	Q9kxg2 escherichia
14	39	72.2	175	10	Q9FSI4	Q9fsi4 hordeum vul
15	39	72.2	202	10	Q9M7J8	Q9m7j8 hordeum vul
16	39	72.2	1118	10	Q93VL6	Q93vl6 phaseolus v
17	38	70.4	107	11	Q9JL84	Q9jl84 mus musculu
18	38	70.4	185	5	Q9Y0V9	Q9y0v9 drosophila
19	38	70.4	185	5	Q8SYA0	Q8sya0 drosophila
20	38	70.4	187	5	Q9W0S5	Q9w0s5 drosophila
21	38	70.4	242	13	Q9PU09	Q9pu09 latimeria c
22	38	70.4	245	13	Q8UUT6	Q8uut6 brachydanio
23	38	70.4	271	16	Q9FCG6	Q9fcg6 streptomyce
24	38	70.4	273	2	Q9KI88	Q9ki88 bacillus ce
25	38	70.4	294	2	Q9KI87	Q9ki87 bacillus ce
26	38	70.4	296	2	Q9KI89	Q9ki89 bacillus ce
27	38	70.4	335	16	Q8U6Z4	Q8u6z4 agrobacteri
28	38	70.4	453	11	Q921W6	Q921w6 mus musculu
29	38	70.4	592	16	Q99X94	Q99x94 staphylococ
30	38	70.4	608	16	Q8XRX5	Q8xrx5 ralstonia s
31	38	70.4	786	16	Q9FBS2	Q9fbs2 streptomyce
32	38	70.4	1027	10	Q9SSE9	Q9sse9 arabidopsis
33	37	68.5	140	2	Q48404	Q48404 klebsiella
34	37	68.5	183	2	Q93JR2	Q93jr2 rhodococcus
35	37	68.5	277	16	Q8YI83	Q8yi83 brucella me
36	37	68.5	363	4	Q96SU1	Q96su1 homo sapien
37	37	68.5	444	5	Q9VD47	Q9vd47 drosophila
38	37	68.5	452	10	Q943G2	Q943g2 oryza sativ
39	37	68.5	464	16	Q92QV6	Q92qv6 rhizobium m
40	37	68.5	486	16	Q9FBN5	Q9fbn5 streptomyce
41	37	68.5	607	2	Q8RQP7	Q8rqp7 streptomyce
42	37	68.5	703	5	Q16944	Q16944 aplysia cal
43	37	68.5	712	5	Q16971	Q16971 aplysia cal
44	36	66.7	175	5	Q9U455	Q9u455 anopheles g
45	36	66.7	214	16	Q92WK3	Q92wk3 rhizobium m

ALIGNMENTS

RESULT 1
Q9UL78
ID Q9UL78 PRELIMINARY; PRT; 109 AA.
AC Q9UL78;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035036; AAD56272.1; -.
DR HSSP; P80362; 1WTL.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGv; 1.
FT NON_TER 1 1
FT NON_TER 109 109
SQ SEQUENCE 109 AA; 11646 MW; 5F675C52EC7EE197 CRC64;

Query Match 75.9%; Score 41; DB 4; Length 109;
Best Local Similarity 88.9%; Pred. No. 4.8;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy       1 QQYGSSPWT 9
           ||||||| |
Db      90 QQYGSSPLT 98
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```
RESULT 2
Q99Y45
ID   Q99Y45      PRELIMINARY;      PRT;   141 AA.
AC   Q99Y45;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Putative ribosomal-protein-alanine acetyltransferase.
GN   SPY1873.
OS   Streptococcus pyogenes.
OC   Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OC   Streptococcaceae; Streptococcus.
OX   NCBI_TaxID=1314;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=SF370 / ATCC 700294 / SEROTYPE M1;
RX   MEDLINE=21192684; PubMed=11296296;
RA   Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,
RA   Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,
RA   Qian Y., Jia H.G., Najar F.Z., Ren Q., Zhu H., Song L., White J.,
RA   Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;
RT   "Complete genome sequence of an M1 strain of Streptococcus pyogenes.";
RL   Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
DR   EMBL; AE006612; AAK34587.1; -.
DR   InterPro; IPR000182; GCN5acetyltransf.
DR   Pfam; PF00583; Acetyltransf; 1.
KW   Transferase; Complete proteome.
SQ   SEQUENCE   141 AA;  16520 MW;  007313989E955E08 CRC64;

  Query Match             75.9%;  Score 41;  DB 16;  Length 141;
  Best Local Similarity   85.7%;  Pred. No. 6.3;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3 YGSSPWT 9
           ||:||||
Db      19 YGTSPWT 25


RESULT 3
O13664
ID   O13664      PRELIMINARY;      PRT;   373 AA.
AC   O13664;
DT   01-JAN-1998 (TrEMBLrel. 05, Created)
DT   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Pi073 protein.
GN   PI073.
OS   Schizosaccharomyces pombe (Fission yeast).
OC   Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC   Schizosaccharomycetales; Schizosaccharomycetaceae;
OC   Schizosaccharomyces.
OX   NCBI_TaxID=4896;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=972 H-;
RX   MEDLINE=20089027; PubMed=10620777;
RA   Machida M., Yamazaki S., Kunihiro S., Tanaka T., Kushida N., Jinno K.,
RA   Haikawa Y., Yamazaki J., Yamamoto S., Sekine M., Oguchi A., Nagai Y.,
RA   Sakai M., Aoki K., Ogura K., Kudoh Y., Kikuchi H., Zhang M.Q.,
RA   Yanagida M.;
RT   "A 38 kb segment containing the cdc2 gene from the left arm of fission
RT   yeast chromosome II: sequence analysis and characterization of the
RT   genomic DNA and cDNAs encoded on the segment.";
RL   Yeast 16:71-80(2000).
DR   EMBL; AB004539; BAA21455.1; -.
DR   InterPro; IPR001680; WD40.
DR   Pfam; PF00400; WD40; 1.
DR   SMART; SM00320; WD40; 1.
DR   PROSITE; PS00678; WD_REPEATS_1; UNKNOWN_1.
DR   PROSITE; PS50082; WD_REPEATS_2; 1.
DR   PROSITE; PS50294; WD_REPEATS_REGION; 1.
KW   Repeat; WD repeat.
SQ   SEQUENCE   373 AA;  43018 MW;  69B6C39E27CFD46E CRC64;

  Query Match             75.9%;  Score 41;  DB 3;  Length 373;
  Best Local Similarity   75.0%;  Pred. No. 18;
  Matches    6;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 QQYGSSPW 8
           ||:| |||
Db     174 QQFGQSPW 181


RESULT 4
O42996
ID   O42996      PRELIMINARY;      PRT;   391 AA.
AC   O42996;
DT   01-JUN-1998 (TrEMBLrel. 06, Created)
DT   01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   WD repeat protein.
GN   SPBC27B12.05.
OS   Schizosaccharomyces pombe (Fission yeast).
OC   Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC   Schizosaccharomycetales; Schizosaccharomycetaceae;
OC   Schizosaccharomyces.
OX   NCBI_TaxID=4896;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=972H-;
RA   Wood V., Rajandream M.A., Barrell B.G., Lauber J., Hilbert H.,
RA   Duesterhoeft A;
RL   Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AL021766; CAA16900.1; -.
DR   InterPro; IPR001680; WD40.
DR   Pfam; PF00400; WD40; 1.
DR   SMART; SM00320; WD40; 1.
DR   PROSITE; PS00678; WD_REPEATS_1; UNKNOWN_1.
DR   PROSITE; PS50082; WD_REPEATS_2; 1.
DR   PROSITE; PS50294; WD_REPEATS_REGION; 1.
KW   Repeat; WD repeat.
SQ   SEQUENCE   391 AA;  44836 MW;  A849BB001264D349 CRC64;

  Query Match             75.9%;  Score 41;  DB 3;  Length 391;
  Best Local Similarity   75.0%;  Pred. No. 18;
  Matches    6;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 QQYGSSPW 8
           ||:| |||
Db     174 QQFGQSPW 181


RESULT 5
Q9J028
ID   Q9J028      PRELIMINARY;      PRT;   414 AA.
AC   Q9J028;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Regulatory protein E2.
OS   rabbit oral papillomavirus.
OC   Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC   Papillomavirus.
OX   NCBI_TaxID=122291;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20219637; PubMed=10753723;
RA   Christensen N.D., Cladel N.M., Reed C.A., Han R.;
RT   "Rabbit oral papillomavirus complete genome sequence and immunity
RT   following genital infection.";
RL   Virology 269:451-461(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Christensen N.D., Cladel N.M., Reed C.A., Han R.;
RL   Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
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OM protein - protein search, using sw model

Run on: April 16, 2003, 16:56:17 ; Search time 7.13684 Seconds
(without alignments)
168.037 Million cell updates/sec

Title: US-09-644-668A-35
Perfect score: 54
Sequence: 1 QQYGSSPWT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_101002:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	54	100.0	9	22	AAB67495	Human light chain
2	54	100.0	108	22	AAG93666	Human anti-Rh(D) a
3	54	100.0	108	22	AAB62770	Human HIV-1 monocl
4	51	94.4	108	15	AAR54307	Anti-HIV gp120 imm
5	51	94.4	108	17	AAW01265	VL region of HIV n
6	51	94.4	108	21	AAY95117	Anti-gp120 antibod
7	51	94.4	108	21	AAY98226	Anti-gp120 antibod
8	51	94.4	235	21	AAY93702	The kappa chain of
9	51	94.4	235	21	AAY93729	The kappa chain of
10	45	83.3	8	15	AAR58530	Light chain CDR3 f
11	45	83.3	8	17	AAR95303	Light chain CDR3 o
12	45	83.3	11	17	AAW10700	Random light chain
13	45	83.3	107	22	AAB62771	Human HIV-1 monocl
14	45	83.3	109	22	AAB62773	Human HIV-1 monocl
15	45	83.3	129	14	AAR38672	vk325-Jk2. Homo s
16	45	83.3	212	23	ABP51681	Human tetanus toxo
17	45	83.3	214	18	AAW45517	NANUC-2 light chai
18	45	83.3	214	18	AAW07615	Ulcerative colitis
19	45	83.3	214	19	AAW64671	Human UC pANCA mon
20	45	83.3	214	20	AAY34039	NANUC-2 antibody l
21	45	83.3	214	21	AAY57337	UC pANCA MAb NANUC
22	44	81.5	9	15	AAR58533	Light chain CDR3 f
23	44	81.5	9	17	AAR95306	Light chain CDR3 o
24	44	81.5	9	22	AAU07472	Synthetic peptide
25	44	81.5	108	22	AAU07490	Synthetic antibody
26	43.5	80.6	109	23	ABB07231	Anti-IL-4 receptor
27	43.5	80.6	109	23	ABB07233	Anti-IL-4 and IL-1
28	43	79.6	107	14	AAR38614	Low-risk modified
29	43	79.6	107	14	AAR41283	Moderate-risk modi
30	43	79.6	107	19	AAW58515	Protein SEQ ID NO:
31	43	79.6	107	19	AAW58505	H65 protein sequen
32	43	79.6	107	19	AAW58478	Humanised anti-CD5
33	43	79.6	108	13	AAR21310	Light chain of M1f
34	43	79.6	109	18	AAW18271	PrP 37 light chain
35	43	79.6	109	20	AAW85910	PrP 37 light chain
36	43	79.6	109	22	AAG65862	Anti-PrP antibody
37	43	79.6	109	23	ABP51796	Anti-prion protein
38	43	79.6	129	14	AAR30880	pXOM2. Mus muscul
39	43	79.6	146	4	AAP30251	Sequence of the le
40	42	77.8	9	14	AAR30158	MAb GAH variable r
41	42	77.8	9	18	AAW24551	CDR #3 of r101-2 l
42	42	77.8	9	21	AAB06351	Randomised VL3 seq
43	42	77.8	9	21	AAB06354	Randomised VL3 seq
44	42	77.8	107	14	AAR30770	Consensus humanise
45	42	77.8	107	22	AAB62087	Human Vl consensus

ALIGNMENTS

RESULT 1
AAB67495
ID AAB67495 standard; peptide; 9 AA.
XX
AC AAB67495;
XX
DT 29-MAY-2001 (first entry)
XX
DE Human light chain complementarity determining region 3 (CDR3).
XX
KW Complementarity determining region; CDR; immune response; antibody;
KW cytotoxic T lymphocyte associated antigen-4; CTLA-4; B7 ligand; cancer;
KW autoimmune disease; infectious disease; inflammation; allergy;
KW rheumatoid arthritis; myasthenia gravis; lupus erythematosus;
KW multiple sclerosis; insulin-dependent diabetes mellitus; inflammation;
KW transplant rejection; graft versus host disease.
XX
OS Homo sapiens.
XX
PN WO200114424-A2.
XX
PD 01-MAR-2001.
XX
PF 24-AUG-2000; 2000WO-US23356.
XX
PR 24-AUG-1999; 99US-0150452.
XX
PA (MEDA-) MEDAREX INC.
XX
PI Korman AJ, Halk EL, Lonberg N;
XX
DR WPI; 2001-202933/20.
XX

PT Novel human sequence antibody that binds to human cytotoxic T
PT lymphocyte associated antigen-4, useful for inducing, augmenting or
PT prolonging immune response to antigen or for suppressing immune
PT response in patient -
XX
PS Claim 30; Page 99; 127pp; English.
XX
CC AAB67490-99 and AAB67501-06 represents complementarity determining
CC regions (CDRs) of human antibodies. The antibodies specifically bind to
CC human cytotoxic T lymphocyte associated antigen-4 (CTLA-4). Such
CC antibodies are used in methods for inducing, augmenting or prolonging
CC an immune response to an antigen in a patient, where the antibodies
CC block binding of human CTLA-4 to human B7 ligands. The antibodies are
CC also useful for treating autoimmune disease in a subject caused or
CC exacerbated by increased activity of T cells and for treating prostate
CC cancer, melanoma or epithelial cancer. A polyvalent or polyclonal
CC antibody preparation comprising two antibodies of the invention are
CC useful for suppressing a immune response in a patient. They are used for
CC treating cancer, infectious diseases and promoting beneficial autoimmune
CC reactions for the treatment of diseases with inflammatory or allergic
CC components. The polyvalent or polyclonal preparations are useful for
CC treating autoimmune diseases such as rheumatoid arthritis, myasthenia
CC gravis and lupus erythematosus, multiple sclerosis, insulin-dependent
CC diabetes mellitus, transplant rejection, and inflammation, graft versus
CC host disease.
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 54; DB 22; Length 9;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQYGSSPWT 9
|||||||||
Db 1 QQYGSSPWT 9

RESULT 2
AAG93666
ID AAG93666 standard; Protein; 108 AA.
XX
AC AAG93666;
XX
DT 14-SEP-2001 (first entry)
XX
DE Human anti-Rh(D) antibody clone SH52 protein sequence.
XX
KW Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;
KW ed blood cell; Rh phenotype; diagnosis; therapeutic.
XX
OS Homo sapiens.
XX
PN US6255455-B1.
XX
PD 03-JUL-2001.
XX
PF 29-JAN-1999; 99US-0240274.
XX
PR 11-OCT-1996; 96US-0028550.
PR 10-APR-1998; 98US-0081380.
PR 27-JUN-1997; 97US-0884045.
XX
PA (UYPE-) UNIV PENNSYLVANIA.
XX
PI Siegel DL;
XX
DR WPI; 2001-388931/41.
DR N-PSDB; AAH68723.
XX
PT New isolated protein, preferably a human anti-Rh(D) antibody for use in
PT diagnostics requiring a human instead of an animal antibody and in
PT therapeutic medicine -
XX
PS Claim 1; Column 70; 162pp; English.
XX
CC The present invention describes an isolated Rh(D) binding protein,
CC preferably a human antibody, (I) having an amino acid sequence comprising
CC one of the sequences (S) given in AAG93558 to AAG93669. (I) has
CC immunostimulant activity, and can be used as an immune system stimulant.
CC (I) can be used in diagnostic and therapeutic medicine. The antibodies
CC are used in diagnostics that require human antibodies instead of animal
CC antibodies, such as determine the Rh phenotype of human red blood cells.
CC AAH68615 to AAH68726 represent the nucleotide sequence which encode
CC AAG93558 to AAG93669. AAG93670 to AAG93697 represent anti-Rh(D) heavy
CC chain CDR3 amino acid sequences which are given in the exemplification
CC of the present invention.
XX
SQ Sequence 108 AA;

Query Match 100.0%; Score 54; DB 22; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.079;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQYGSSPWT 9
|||||||||
Db 89 QQYGSSPWT 97

RESULT 3
AAB62770
ID AAB62770 standard; Protein; 108 AA.
XX
AC AAB62770;
XX
DT 03-APR-2001 (first entry)
XX
DE Human HIV-1 monoclonal antibody SEQ ID NO: 69.
XX
KW Human immunodeficiency virus-1; HIV-1; human monoclonal antibody;
KW envelope glycoprotein; gp120; diagnosis.
XX
OS Homo sapiens.
XX
PN WO200100678-A1.
XX
PD 04-JAN-2001.
XX
PF 23-JUN-2000; 2000WO-US17327.
XX
PR 30-JUN-1999; 99US-0141701.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Watkins BA, Reitz MS;
XX
DR WPI; 2001-112438/12.
DR N-PSDB; AAF29071.
XX
PT Novel human monoclonal antibody immunoreactive with human
PT immunodeficiency virus-1 glycoprotein gp120, useful for detecting HIV-1
PT in biological sample and providing passive immunotherapy to HIV-1
PT infected mammal -
XX
PS Claim 1; Page 66; 81pp; English.
XX
CC The present invention provides the protein and coding sequences for the
CC variable regions of human monoclonal antibodies which are immunoreactive
CC with human immunodeficiency virus-1 (HIV-1) envelope glycoprotein gp120.
CC These can be used in diagnosis and therapy of HIV-1 infection.
XX
SQ Sequence 108 AA;

Query Match 100.0%; Score 54; DB 22; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.079;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 QQYGSSPWT 9
          |||||||||
Db     89 QQYGSSPWT 97
```

```
RESULT 4
AAR54307
ID   AAR54307 standard; protein; 108 AA.
XX
AC   AAR54307;
XX
DT   10-NOV-1994  (first entry)
XX
DE   Anti-HIV gp120 immunoglobulin light chain variable region b24.
XX
KW   Human immunodeficiency virus; HIV1; glycoprotein gp120; epitope;
KW   neutralisation; monoclonal antibody; kappa light chain;
KW   variable region; framework; complementarity determining region.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Region          1..21
FT                   /label= FR1
FT   Region          22..33
FT                   /label= CDR1
FT   Region          34..48
FT                   /label= FR2
FT   Region          49..55
FT                   /label= CDR2
FT   Region          56..87
FT                   /label= FR3
FT   Region          88..96
FT                   /label= CDR3
FT   Region          97..108
FT                   /label= FR4
XX
PN   WO9407922-A.
XX
PD   14-APR-1994.
XX
PF   30-SEP-1993;   93WO-US09328.
XX
PR   30-SEP-1992;   92US-0954148.
XX
PA   (SCRI ) SCRIPPS RES INST.
XX
PI   Barbas CF,  Burton DR,  Lerner RA;
XX
DR   WPI; 1994-135516/16.
XX
PT   New human monoclonal antibodies neutralising HIV - react with
PT   gp120 or gp41 and nucleic acid encoding them, useful for in vivo
PT   or in vitro diagnosis and for passive immuno-therapy
XX
PS   Example; Page 177-178; 248pp; English.
XX
CC   Lymphocyte mRNA was converted to cDNA and subjected to PCR
CC   amplification using primers specific for heavy and light chain
CC   variable regions. The amplification products were inserted into a
CC   dicistronic vector to produce a library of fragments. E.coli XL1
CC   Blue cells were transformed with the library. Filamentous phage were
CC   produced which expressed the MAb regions on their surface. Panning
CC   with gp120 and gp41 resulted in the recovery of immunoreactive
CC   clones. The light chain VK region sequence AAR54307 is from a gp120-
CC   specific clone.
XX
SQ   Sequence   108 AA;

  Query Match             94.4%;  Score 51;  DB 15;  Length 108;
  Best Local Similarity   88.9%;  Pred. No. 0.26;
  Matches    8;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy      1 QQYGSSPWT 9
          ||||:||||
Db     88 QQYGTSPWT 96
```

```
RESULT 5
AAW01265
ID   AAW01265 standard; Protein; 108 AA.
XX
AC   AAW01265;
XX
DT   28-JAN-1997  (first entry)
XX
DE   VL region of HIV neutralising MAb, clone b24.
XX
KW   Heavy chain; light chain; variable region; VH; monoclonal antibody;
KW   MAb; HIV; human immunodeficiency virus; glycoprotein; gp120; clone;
KW   virus infectivity assay; precursor gp160; immunocompetence; human;
KW   anti-HIV antibody; detection; HIV infection.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
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FT                   /label= FR1
FT   Region          22..33
FT                   /label= CDR1
FT   Region          34..48
FT                   /label= FR2
FT   Region          49..55
FT                   /label= CDR2
FT   Region          56..87
FT                   /label= FR3
FT   Region          88..96
FT                   /label= CDR3
FT   Region          97..108
FT                   /label= FR4
XX
PN   WO9602273-A1.
XX
PD   01-FEB-1996.
XX
PF   11-JUL-1995;   95WO-US08743.
XX
PR   18-JUL-1994;   94US-0276852.
XX
PA   (SCRI ) SCRIPPS RES INST.
XX
PI   Barbas CF,  Burton DR,  Lerner RA;
XX
DR   WPI; 1996-179601/18.
XX
PT   Monoclonal antibody binding to V1/V2 loop of HIV gp120 - used in
PT   passive immuno:therapy and detection of HIV infection.
XX
PS   Example; Fig 11; 366pp; English.
XX
CC   The sequences given in AAW01261-92 represent the light chain variable
CC   regions (VL) of a series of monoclonal antibodies (MAb's) which are
CC   immunoreactive with HIV glycoprotein gp120 and are capable of
CC   neutralising HIV.  This sequence represents the sequence of the JK1
CC   gene clone, b24.  A MAb containing this VL sequence has the capacity
CC   to reduce HIV infectivity titre in an in vivo virus infectivity assay
CC   by 50 % at a concentration of less than 700 ng of antibody/ml, and
CC   binds mature gp120 preferentially over the precursor gp160.  The MAb
CC   may be used for determining immunocompetence of a human anti-HIV
CC   antibody and in the detection of HIV infection.
XX
SQ   Sequence   108 AA;

  Query Match             94.4%;  Score 51;  DB 17;  Length 108;
  Best Local Similarity   88.9%;  Pred. No. 0.26;
  Matches    8;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy      1 QQYGSSPWT 9
          ||||:||||
Db     88 QQYGTSPWT 96
```

RESULT 6
AAY95117
ID AAY95117 standard; Protein; 108 AA.
XX
AC AAY95117;
XX
DT 30-JUN-2000 (first entry)
XX
DE Anti-gp120 antibody light chain variable region from clone b24.
XX
KW Anti-human immunodeficiency virus type 1 antibody; HIV-1; neutralise;
KW reduce HIV infection; diagnosis; immunotherapy; HIV induced disease;
KW glycoprotein 120; gp120; glycoprotein 41; gp41; monoclonal antibody.
XX
OS Homo sapiens.
XX
PN AU9948756-A.
XX
PD 17-FEB-2000.
XX
PF 16-SEP-1999; 99AU-0048756.
XX
PR 16-SEP-1999; 99AU-0048756.
XX
PA (SCRI) SCRIPPS RES INST.
XX
PI Burton DR, Barbas CF, Lerner RA;
XX
DR WPI; 2000-293393/26.
XX
PT Novel human monoclonal antibodies which immunoreact with and neutralise
PT human immunodeficiency virus useful for treating HIV infections -
XX
PS Example 9; Figure 11; 366pp; English.
XX
CC The present sequence represents a fragment of an anti-human
CC immunodeficiency virus type 1 (HIV-1) antibody. The invention relates to
CC a human whole immunoglobulin (Ig) molecule which immunoreacts with HIV
CC mature glycoprotein gp120 preferentially over HIV precursor glycoprotein
CC gp160 and neutralises HIV and which reduces HIV infectivity titre in an
CC in vitro virus infectivity assay by 50%, at a concentration of less than
CC 700 ng/ml. The antibodies are used as reagents for the diagnosis and
CC immunotherapy of HIV induced disease. They are useful as neutralising
CC field isolates and provide useful information regarding the
CC immunocompetence of an immune response in HIV infected patients. The
CC monoclonal antibodies are useful for producing anti-idiotypic antibodies
CC which can be used to screen human monoclonal antibodies to identify
CC whether the antibody has the same binding specificity as the antibodies
CC of the invention. The neutralising antibodies define new epitopes on the
CC HIV gp120 and gp41 glycoproteins, thus increasing the availability of new
CC immunotherapeutic human monoclonal antibodies. A major advantages of the
CC monoclonal antibodies derives from the fact that they are encoded by a
CC human polynucleotides sequence. Thus in vivo use of the monoclonal
CC antibodies for diagnosis and immunotherapy of HIV induced disease greatly
CC reduces the problems of significant host immune response to the passively
CC administered antibodies which is a problem commonly encountered when
CC monoclonal antibodies of xenogeneic or chimeric derivation are utilized.
CC An additional major advantage of the monoclonal antibodies described
CC derives from the fact that they immunoreact with a unique determinant
CC present on mature HIV glycoprotein gp120. This class of antibodies is
CC particularly effective at neutralising field isolates of HIV.
XX
SQ Sequence 108 AA;

```
  Query Match             94.4%;  Score 51;  DB 21;  Length 108;
  Best Local Similarity   88.9%;  Pred. No. 0.26;
  Matches    8;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;
```


```
Qy      1 QQYGSSPWT 9
          ||||:||||
Db     88 QQYGTSPWT 96
```


RESULT 7
AAY98226
ID AAY98226 standard; Protein; 108 AA.
XX
AC AAY98226;
XX
DT 04-JUL-2000 (first entry)
XX
DE Anti-gp120 antibody light chain variable region from clone b24.
XX
KW Antibody; anti-HIV monoclonal antibody; glycoprotein-120;
KW human immunodeficiency virus type 1; HIV-1; infectivity titre;
KW passive immunotherapy; reduce severity; HIV-induced disease;
KW immunocompetence; active immunisation.
XX
OS Homo sapiens.
XX
PN AU9948754-A.
XX
PD 17-FEB-2000.
XX
PF 16-SEP-1999; 99AU-0048754.
XX
PR 16-SEP-1999; 99AU-0048754.
XX
PA (SCRI) SCRIPPS RES INST.
XX
PI Burton DR, Barbas CF, Lerner RA;
XX
DR WPI; 2000-246867/22.
XX
PT Human neutralizing monoclonal antibodies to human immunodeficiency
PT virus (HIV) used for providing passive immunotherapy to HIV are
PT specific for glycoprotein-120 -
XX
PS Example 9; Figure 11; 374pp; English.
XX
CC This sequence represents a fragment of the antibodies of the invention.
CC The invention relates to the production of an anti-HIV (human
CC immunodeficiency virus) glycoprotein (gp)-120 monoclonal antibody
CC capable of reducing an HIV infectivity titre in an in vitro virus
CC infectivity assay by 50% at a concentration of less than 70 ng/ml. The
CC method for the production of the antibody comprises:
CC (a) providing a first polynucleotide encoding a heavy chain
CC immunoglobulin amino acid sequence (which does not comprise the sequence
CC represented by AAY98206) and a second polynucleotide encoding a light
CC chain immunoglobulin amino acid sequence;
CC (b) inserting the first and second polynucleotide sequences into a host
CC cell;
CC (c) maintaining the host cell in conditions which allow the amino acid
CC sequences encoded by the polynucleotides to be expressed in the host
CC cell; and
CC (d) isolating the antibody comprising the heavy and light chain
CC immunoglobulin amino acid sequences from the host cell.
CC The anti-HIV gp-120 monoclonal antibody is used for providing passive
CC immunotherapy to HIV in a human. They can be administered to high-risk
CC patients to reduce the likelihood and/or severity of HIV-induced disease
CC and to patients who are already HIV-infected. The antibodies are used
CC for neutralising field isolates which provides information about the
CC immunocompetence of an immune response in HIV patients, for detecting
CC HIV in a biological fluid or tissue sample e.g. by radioimmunoassay, for
CC producing anti-idiotypic antibodies which can be used for active
CC immunisation and to screen human monoclonal antibodies to identify those
CC with the same binding specificity and to monitor the course of HIV
CC disease therapy by measuring the changes in concentration of HIV present
CC in the body or in body fluids by immunoassay. The anti-HIV gp-120
CC monoclonal antibodies are encoded by a human polynucleotide sequence and

GenCore version 5.1.4_p5_4578

OM protein - protein search, using sw model

Run on: April 16, 2003, 17:21:54 ; Search time 2.65263 Seconds
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Searched: 288829 seqs, 75613885 residues

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	54	100.0	108	9	US-09-848-798-178	Sequence 178, App
2	45	83.3	212	9	US-10-006-593-118	Sequence 118, App
3	43	79.6	109	10	US-09-943-906-74	Sequence 74, Appl
4	42	77.8	108	10	US-09-056-160B-12	Sequence 12, Appl
5	42	77.8	109	10	US-09-811-123-6	Sequence 6, Appli
6	42	77.8	249	9	US-10-237-667-18	Sequence 18, Appl
7	42	77.8	249	9	US-10-237-708-18	Sequence 18, Appl
8	42	77.8	249	9	US-10-237-866-18	Sequence 18, Appl
9	42	77.8	249	9	US-10-237-871-18	Sequence 18, Appl
10	42	77.8	249	10	US-09-984-186-18	Sequence 18, Appl
11	41	75.9	150	9	US-09-782-397-5	Sequence 5, Appli
12	41	75.9	287	9	US-09-782-397-17	Sequence 17, Appl
13	41	75.9	304	9	US-09-782-397-14	Sequence 14, Appl
14	40	74.1	9	10	US-09-056-160B-125	Sequence 125, App
15	40	74.1	9	10	US-09-828-708-52	Sequence 52, Appl
16	40	74.1	9	10	US-09-828-708-56	Sequence 56, Appl
17	40	74.1	105	10	US-09-828-708-3	Sequence 3, Appli
18	40	74.1	105	10	US-09-828-708-7	Sequence 7, Appli
19	40	74.1	107	8	US-08-844-215-10	Sequence 10, Appl
20	40	74.1	107	8	US-08-844-215-12	Sequence 12, Appl
21	40	74.1	253	9	US-09-880-748-1499	Sequence 1499, Ap
22	40	74.1	261	9	US-10-231-013-13	Sequence 13, Appl
23	39	72.2	9	10	US-09-056-160B-6	Sequence 6, Appli
24	39	72.2	107	10	US-09-056-160B-13	Sequence 13, Appl
25	39	72.2	107	10	US-09-056-160B-15	Sequence 15, Appl
26	39	72.2	108	9	US-10-153-159-2	Sequence 2, Appli
27	39	72.2	108	9	US-10-153-159-4	Sequence 4, Appli
28	39	72.2	108	9	US-10-153-159-16	Sequence 16, Appl
29	39	72.2	108	9	US-10-153-176-2	Sequence 2, Appli
30	39	72.2	108	9	US-10-153-176-4	Sequence 4, Appli
31	39	72.2	108	9	US-10-153-176-16	Sequence 16, Appl
32	39	72.2	108	10	US-09-056-160B-8	Sequence 8, Appli
33	39	72.2	108	10	US-09-056-160B-10	Sequence 10, Appl
34	39	72.2	108	10	US-09-056-160B-126	Sequence 126, App
35	39	72.2	110	10	US-09-056-160B-103	Sequence 103, App
36	39	72.2	110	10	US-09-056-160B-105	Sequence 105, App
37	39	72.2	110	10	US-09-056-160B-107	Sequence 107, App
38	39	72.2	110	10	US-09-056-160B-109	Sequence 109, App
39	39	72.2	110	10	US-09-056-160B-111	Sequence 111, App
40	39	72.2	110	10	US-09-056-160B-113	Sequence 113, App
41	39	72.2	110	10	US-09-056-160B-115	Sequence 115, App
42	39	72.2	110	10	US-09-056-160B-117	Sequence 117, App
43	39	72.2	154	9	US-09-925-299-1226	Sequence 1226, Ap
44	39	72.2	154	10	US-09-925-299-1226	Sequence 1226, Ap
45	39	72.2	237	10	US-09-056-160B-100	Sequence 100, App

ALIGNMENTS

RESULT 1
US-09-848-798-178
; Sequence 178, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/848,798
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 178
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH52
US-09-848-798-178

Query Match 100.0%; Score 54; DB 9; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.022;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQYGSSPWT 9
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Db 89 QQYGSSPWT 97

RESULT 2
US-10-006-593-118
; Sequence 118, Application US/10006593
; Publication No. US20030049683A1
; GENERAL INFORMATION:
; APPLICANT: Bowdish, Katherine S.
; APPLICANT: Frederickson, Shana
; APPLICANT: Renshaw, Mark

; TITLE OF INVENTION: RATIONALLY DESIGNED ANTIBODIES
; FILE REFERENCE: 1087-2
; CURRENT APPLICATION NUMBER: US/10/006,593
; CURRENT FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: US 60/251,448
; PRIOR FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: US 60/288,889
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/294,068
; PRIOR FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 118
; LENGTH: 212
; TYPE: PRT
; ORGANISM: human
US-10-006-593-118

Query Match 83.3%; Score 45; DB 9; Length 212;
Best Local Similarity 87.5%; Pred. No. 1.5;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QQYGSSPW 8
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Db 88 QQYGGSPW 95

RESULT 3
US-09-943-906-74
; Sequence 74, Application US/09943906
; Patent No. US20020150571A1
; GENERAL INFORMATION:
; APPLICANT: Prusiner, Stanley B.
; Williamson, R. Anthony
; Burton, Dennis R.
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR NATIVE PrP
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 2200 Sand Hill Road
; CITY: Menlo Park
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/943,906
; FILING DATE: 30-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/550,374
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Bozicevic, Karl
; REGISTRATION NUMBER: 28,807
; REFERENCE/DOCKET NUMBER: 06510/059001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-854-5277
; TELEFAX: 415-854-0875
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 74:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 74:
US-09-943-906-74

Query Match 79.6%; Score 43; DB 10; Length 109;
Best Local Similarity 87.5%; Pred. No. 1.8;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QYGSSPWT 9
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Db 90 QYASSPWT 97

RESULT 4
US-09-056-160B-12
; Sequence 12, Application US/09056160B
; Patent No. US20020032315A1
; GENERAL INFORMATION:
; APPLICANT: Baca, Manuel
; APPLICANT: Wells, James A.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Lowman, Henry B.
; APPLICANT: Chen, Yvonne M.
; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
; NUMBER OF SEQUENCES: 131
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/056,160B
; FILING DATE: 06-Apr-1998
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/054,856
; FILING DATE: 06-AUG-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hasak, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: P1093R2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1896
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-09-056-160B-12

Query Match 77.8%; Score 42; DB 10; Length 108;
Best Local Similarity 77.8%; Pred. No. 2.6;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QQYGSSPWT 9
||| | |||
Db 89 QQYNSLPWT 97

RESULT 5
US-09-811-123-6
; Sequence 6, Application US/09811123
; Patent No. US20020001587A1
; GENERAL INFORMATION:
; APPLICANT: Sharon Erickson
; APPLICANT: Ralph Schwall
; APPLICANT: Mark Sliwkowski
; TITLE OF INVENTION: METHODS OF TREATMENT USING ANTI-ErbB

GenCore version 5.1.4_p5_4578

OM protein - protein search, using sw model

Run on: April 16, 2003, 17:15:40 ; Search time 2.30526 Seconds
(without alignments)
114.870 Million cell updates/sec

Title: US-09-644-668A-35
Perfect score: 54
Sequence: 1 QQYGSSPWT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	54	100.0	108	4	US-09-240-274-178	Sequence 178, App
	51	94.4	108	1	US-08-276-852-86	Sequence 86, Appl
	51	94.4	108	1	US-08-899-575-86	Sequence 86, Appl
	51	94.4	108	1	US-08-899-575-86	Sequence 86, Appl
5	51	94.4	108	5	PCT-US95-08743-86	Sequence 86, Appl
6	49	90.7	107	2	US-08-652-558-49	Sequence 49, Appl
7	45	83.3	8	1	US-08-300-386A-47	Sequence 47, Appl
8	45	83.3	8	3	US-08-931-645-47	Sequence 47, Appl
9	45	83.3	8	5	PCT-US94-01258-47	Sequence 47, Appl
10	45	83.3	8	5	PCT-US95-11235-47	Sequence 47, Appl
11	45	83.3	9	2	US-08-350-260A-503	Sequence 503, App
12	45	83.3	11	1	US-08-209-525-26	Sequence 26, Appl
13	45	83.3	214	2	US-08-480-753-6	Sequence 6, Appli
14	45	83.3	214	3	US-09-041-889-11	Sequence 11, Appl
15	45	83.3	214	3	US-08-837-058-11	Sequence 11, Appl
16	44	81.5	9	1	US-08-300-386A-50	Sequence 50, Appl
17	44	81.5	9	3	US-08-931-645-50	Sequence 50, Appl
18	44	81.5	9	5	PCT-US94-01258-50	Sequence 50, Appl
19	44	81.5	9	5	PCT-US95-11235-50	Sequence 50, Appl
20	43	79.6	107	1	US-08-425-336-123	Sequence 123, App
21	43	79.6	107	1	US-08-425-336-125	Sequence 125, App
22	43	79.6	107	1	US-08-488-113B-123	Sequence 123, App
23	43	79.6	107	1	US-08-488-113B-125	Sequence 125, App
24	43	79.6	107	1	US-08-477-484B-123	Sequence 123, App
25	43	79.6	107	1	US-08-477-484B-125	Sequence 125, App
26	43	79.6	107	1	US-08-107-669D-26	Sequence 26, Appl
27	43	79.6	107	1	US-08-107-669D-27	Sequence 27, Appl
28	43	79.6	107	1	US-08-107-669D-65	Sequence 65, Appl
29	43	79.6	107	1	US-08-472-788A-26	Sequence 26, Appl
30	43	79.6	107	1	US-08-472-788A-27	Sequence 27, Appl
31	43	79.6	107	1	US-08-472-788A-87	Sequence 87, Appl
32	43	79.6	107	2	US-08-477-531B-26	Sequence 26, Appl
33	43	79.6	107	2	US-08-477-531B-27	Sequence 27, Appl
34	43	79.6	107	2	US-08-477-531B-65	Sequence 65, Appl
35	43	79.6	107	2	US-08-646-360-123	Sequence 123, App
36	43	79.6	107	2	US-08-646-360-125	Sequence 125, App
37	43	79.6	107	2	US-08-082-842A-26	Sequence 26, Appl
38	43	79.6	107	2	US-08-082-842A-27	Sequence 27, Appl
39	43	79.6	107	2	US-08-082-842A-87	Sequence 87, Appl
40	43	79.6	107	4	US-08-839-765-123	Sequence 123, App
41	43	79.6	107	4	US-08-839-765-125	Sequence 125, App
42	43	79.6	107	4	US-09-136-389-123	Sequence 123, App
43	43	79.6	107	4	US-09-136-389-125	Sequence 125, App
44	43	79.6	107	4	US-09-610-838-123	Sequence 123, App
45	43	79.6	107	4	US-09-610-838-125	Sequence 125, App

ALIGNMENTS

RESULT 1
US-09-240-274-178
; Sequence 178, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 178
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH52
US-09-240-274-178

Query Match 100.0%; Score 54; DB 4; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQYGSSPWT 9
||||||||
Db 89 QQYGSSPWT 97

RESULT 2
US-08-276-852-86
; Sequence 86, Application US/08276852
; Patent No. 5652138
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,
; STREET: Mail Drop TPC8

```
;       CITY:  La Jolla
;       STATE:  CA
;       COUNTRY:  USA
;       ZIP:  92037
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/276,852
;       FILING DATE:  18-JUL-1994
;       CLASSIFICATION:  514
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/178,302
;       FILING DATE:  30-SEP-1993
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/954,148
;       FILING DATE:  30-SEP-1992
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Fitting, Thomas
;       REGISTRATION NUMBER:  34,163
;       REFERENCE/DOCKET NUMBER:  SCR1452P
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  619-554-2937
;       TELEFAX:  619-554-6312
;   INFORMATION FOR SEQ ID NO:  86:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  108 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-08-276-852-86

  Query Match             94.4%;  Score 51;  DB 1;  Length 108;
  Best Local Similarity   88.9%;  Pred. No. 0.037;
  Matches    8;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 QQYGSSPWT 9
            ||||:||||
Db      88 QQYGTSPWT 96


RESULT 3
US-08-899-575-86
; Sequence 86, Application US/08899575
; Patent No. 5770440
; GENERAL INFORMATION:
;   APPLICANT:  Burton, Dennis R
;   APPLICANT:  Barbas, Carlos F
;   APPLICANT:  Lerner, Richard A
;   TITLE OF INVENTION:  HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
;   TITLE OF INVENTION:  TO HUMAN IMMUNODEFICIENCY VIRUS
;   NUMBER OF SEQUENCES:  170
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  The Scripps Research Institute, Office of
;     ADDRESSEE:  Patent Counsel
;     STREET:  10666 No. 5770440th Torrey Pines Road, Suite 220,
;     STREET:  Mail Drop TPC8
;     CITY:  La Jolla
;     STATE:  CA
;     COUNTRY:  USA
;     ZIP:  92037
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Floppy disk
;     COMPUTER:  IBM PC compatible
;     OPERATING SYSTEM:  PC-DOS/MS-DOS
;     SOFTWARE:  PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/08/899,575
;     FILING DATE:  24-JUL-1997
;     CLASSIFICATION:  435
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  US 08/276,852
;     FILING DATE:  18-JUL-1994
;     APPLICATION NUMBER:  US 08/178,302
;     FILING DATE:  30-SEP-1993
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  US 07/954,148
;     FILING DATE:  30-SEP-1992
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  Fitting, Thomas
;     REGISTRATION NUMBER:  34,163
;     REFERENCE/DOCKET NUMBER:  SCR1452P
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  619-554-2937
;     TELEFAX:  619-554-6312
; INFORMATION FOR SEQ ID NO:  86:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH:  108 amino acids
;     TYPE:  amino acid
;     TOPOLOGY:  linear
;   MOLECULE TYPE:  protein
US-08-899-575-86

  Query Match             94.4%;  Score 51;  DB 1;  Length 108;
  Best Local Similarity   88.9%;  Pred. No. 0.037;
  Matches    8;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 QQYGSSPWT 9
            ||||:||||
Db      88 QQYGTSPWT 96


RESULT 4
US-08-899-575-86
; Sequence 86, Application US/08899575
; Patent No. 5804440
; GENERAL INFORMATION:
;   APPLICANT:  Burton, Dennis R
;   APPLICANT:  Barbas, Carlos F
;   APPLICANT:  Lerner, Richard A
;   TITLE OF INVENTION:  HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
;   TITLE OF INVENTION:  TO HUMAN IMMUNODEFICIENCY VIRUS
;   NUMBER OF SEQUENCES:  170
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  The Scripps Research Institute, Office of
;     ADDRESSEE:  Patent Counsel
;     STREET:  10666 No. 5804440th Torrey Pines Road, Suite 220,
;     STREET:  Mail Drop TPC8
;     CITY:  La Jolla
;     STATE:  CA
;     COUNTRY:  USA
;     ZIP:  92037
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Floppy disk
;     COMPUTER:  IBM PC compatible
;     OPERATING SYSTEM:  PC-DOS/MS-DOS
;     SOFTWARE:  PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/08/899,575
;     FILING DATE:  24-JUL-1997
;     CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  US 08/276,852
;     FILING DATE:  18-JUL-1994
;     APPLICATION NUMBER:  US 08/178,302
;     FILING DATE:  30-SEP-1993
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  US 07/954,148
;     FILING DATE:  30-SEP-1992
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  Fitting, Thomas
;     REGISTRATION NUMBER:  34,163
;     REFERENCE/DOCKET NUMBER:  SCR1452P
;   TELECOMMUNICATION INFORMATION:
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GenCore version 5.1.4_p5_4578

OM protein - protein search, using sw model

Run on: April 16, 2003, 17:11:36 ; Search time 2.77895 Seconds
(without alignments)
311.344 Million cell updates/sec

Title: US-09-644-668A-37
Perfect score: 58
Sequence: 1 TGWLGPFDY 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
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2	42	72.4	970	2	F64230	spore germination
3	41	70.7	286	2	T03434	probable transport
	41	70.7	286	2	AE3245	hypothetical prote
	41	70.7	328	2	T11938	NADH2 dehydrogenas
	40	69.0	214	2	AG3525	hydrolase family p
7	39.5	68.1	606	2	JC5604	ABC-transporting p
8	39	67.2	365	2	I38720	hFcRn - human
9	39	67.2	401	2	S76788	histidine-tRNA lig
10	39	67.2	401	2	H75554	NifS-related prote
11	39	67.2	646	2	T09906	hypothetical prote
12	39	67.2	887	2	S73768	MG277 homolog F11_
13	38	65.5	143	2	S17939	xpsG protein - Xan
14	38	65.5	344	2	S62765	NADH2 dehydrogenas
15	37	63.8	69	2	B45252	PilV variable regi
16	37	63.8	170	2	S33553	beta-fructofuranos
17	37	63.8	213	2	S68213	Ig heavy chain (Ma
18	37	63.8	377	2	AH3328	NAD(FAD)-utilizing
19	37	63.8	393	2	E87432	conserved hypothet
20	37	63.8	394	2	AF2650	conserved hypothet
21	37	63.8	398	2	A82366	conserved hypothet
22	37	63.8	398	2	AH0482	conserved hypothet
23	37	63.8	400	2	G65146	hypothetical 43.8
24	37	63.8	400	2	D91174	hypothetical prote
25	37	63.8	400	2	D86020	hypothetical prote
26	37	63.8	400	2	AH0988	probable exported
27	37	63.8	401	2	G64161	hypothetical prote
28	37	63.8	420	2	E97432	hypothetical prote
29	37	63.8	430	2	B26421	shufflon A' - Esch
30	37	63.8	473	2	T06167	beta-fructofuranos
31	37	63.8	788	2	I51530	integrin beta-3 su
32	37	63.8	968	2	E90481	alpha-mannosidase
33	36	62.1	106	2	E72239	hypothetical prote
34	36	62.1	125	2	S24703	Ig heavy chain V6
35	36	62.1	254	2	F70961	hypothetical prote
36	36	62.1	311	2	AB1880	hypothetical prote
37	36	62.1	314	2	H88991	protein K08D9.1 [i
38	36	62.1	346	2	F82349	ADP-heptose-LPS he
39	36	62.1	372	2	S60207	fomF protein - Str
40	36	62.1	408	2	AC2188	hypothetical prote
41	36	62.1	540	2	AG2161	GMP synthase (glut
42	36	62.1	542	2	S76358	GMP synthase (glut
43	36	62.1	566	1	YDBPA7	DNA primase - phag
44	36	62.1	566	2	S07508	DNA primase - phag
45	36	62.1	694	2	S56060	long-chain-fatty-a

ALIGNMENTS

RESULT 1
I56197
Fc gamma (IgG) receptor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 05-Nov-1999
C;Accession: I56197; I49661
R;Ahouse, J.J.; Hagerman, C.L.; Mittal, P.; Gilbert, D.J.; Copeland, N.G.; Jenkins, N.A.
J. Immunol. 151, 6076-6088, 1993
A;Title: Mouse MHC class I-like Fc receptor encoded outside the MHC.
A;Reference number: I56197; MUID:94065162; PMID:7504013
A;Accession: I56197
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-365 <RES>
A;Cross-references: GB:L17022; NID:g293385; PIDN:AAA16904.1; PID:g293386
R;Kandil, E.; Noguchi, M.; Ishibashi, T.; Kasahara, M.
J. Immunol. 154, 5907-5918, 1995
A;Title: Structural and phylogenetic analysis of the MHC class I-like Fc receptor gene.
A;Reference number: I49661; MUID:95270984; PMID:7538537
A;Accession: I49661
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-72,'M',74-365 <RE2>
A;Cross-references: GB:D37874; NID:g1009353; PIDN:BAA07111.1; PID:g1009354
C;Genetics:
A;Gene: FcRn
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
C;Keywords: immunoglobulin receptor

Query Match 74.1%; Score 43; DB 2; Length 365;
Best Local Similarity 77.8%; Pred. No. 5.4;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy       1 TGWLGPFDY 9
            ||||||  |
Db      48 TGWLGPQQY 56
```

RESULT 2
F64230
spore germination apparatus protein (gerBB) homolog - Mycoplasma genitalium
C;Species: Mycoplasma genitalium
C;Date: 17-Nov-1995 #sequence_revision 17-Nov-1995 #text_change 21-Jul-2000
C;Accession: F64230
R;Fraser, C.M.; Gocayne, J.D.; White, O.; Adams, M.D.; Clayton, R.A.; Fleischmann, R.D.; M.; Fuhrmann, J.; Nguyen, D.; Utterback, T.R.; Saudek, D.M.; Phillips, C.A.; Merrick, J.M., C.A.; Venter, J.C.
Science 270, 397-403, 1995
A;Title: The minimal gene complement of Mycoplasma genitalium.
A;Reference number: A64200; MUID:96026346; PMID:7569993
A;Accession: F64230
A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA
A;Residues: 1-970 <TIGR>
A;Cross-references: GB:U39707; GB:L43967; NID:g3844865; PIDN:AAC71499.1; PID:g1045972; T
A;Experimental source: strain G-37
C;Genetics:
A;Genetic code: SGC3
A;Start codon: GTG

Query Match 72.4%; Score 42; DB 2; Length 970;
Best Local Similarity 75.0%; Pred. No. 23;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GWLGPFDY 9
||| ||:|
Db 932 GWLSPFNY 939

RESULT 3
T03434
pr[illegible]e transport protein accE - Agrobacterium tumefaciens plasmid pTiC58
C;[illegible]es: Agrobacterium tumefaciens
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 08-Oct-1999
C;Accession: T03434
R;Piper, K.R.; Beck von Bodman, S.; Cook, D.M.; Hwang, I.; Kim, H.; Farrand, S.K.
submitted to the EMBL Data Library, May 1998
A;Reference number: Z14943
A;Accession: T03434
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-286 <PIP>
A;Cross-references: EMBL:AF010180; NID:g3153171; PIDN:AAC17201.1; PID:g3153181
C;Genetics:
A;Gene: accE
A;Genome: plasmid pTiC58
C;Superfamily: oligopeptide permease protein oppB

Query Match 70.7%; Score 41; DB 2; Length 286;
Best Local Similarity 85.7%; Pred. No. 9.4;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 WLGPFDY 9
|| ||||
Db 43 WLAPFDY 49

RESULT 4
AE3245
hyp[illegible]hetical protein accE [imported] - Agrobacterium tumefaciens (strain C58, Dupont) pl
C;[illegible]es: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 01-Feb-2002
C;Accession: AE3245
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I
erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; PMID:11743193
A;Accession: AE3245
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-286 <KUR>
A;Cross-references: GB:AE008690; PIDN:AAL46379.1; PID:g17744171; GSPDB:GN00189
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: accE
A;Genome: plasmid
C;Superfamily: oligopeptide permease protein oppB

Query Match 70.7%; Score 41; DB 2; Length 286;
Best Local Similarity 85.7%; Pred. No. 9.4;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 WLGPFDY 9
|| ||||
Db 43 WLAPFDY 49

RESULT 5
T11938
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 1 - Prototheca wickerhamii mitoch
C;Species: mitochondrion Prototheca wickerhamii
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 03-Jun-2002
C;Accession: T11938
R;Wolff, G.; Plante, I.; Lang, B.F.; Kueck, U.; Burger, G.
J. Mol. Biol. 237, 75-86, 1994
A;Title: Complete sequence of the mitochondrial DNA of the chlorophyte alga Protothec
A;Reference number: Z17373; MUID:94180393; PMID:8133522
A;Accession: T11938
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-328 <WOL>
A;Cross-references: EMBL:U02970; NID:g467843; PID:g467870; PIDN:AAD12657.1
A;Experimental source: strain 263-11
C;Genetics:
A;Genome: mitochondrion
A;Note: nad1
C;Superfamily: NADH dehydrogenase (ubiquinone) chain 1
C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylatic

Query Match 70.7%; Score 41; DB 2; Length 328;
Best Local Similarity 75.0%; Pred. No. 11;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GWLGPFDY 9
||| |||:
Db 253 GWLPPFDF 260

RESULT 6
AG3525
hydrolase family protein BMEII0129 [imported] - Brucella melitensis (strain 16M)
C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
C;Accession: AG3525
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanov
.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Let
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melit
A;Reference number: AD3252; PMID:11756688
A;Accession: AG3525
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-214 <KUR>
A;Cross-references: GB:AE008918; PIDN:AAL53370.1; PID:g17984261; GSPDB:GN00191
A;Experimental source: strain 16M
C;Genetics:
A;Gene: BMEII0129
A;Map position: II

Query Match 69.0%; Score 40; DB 2; Length 214;
Best Local Similarity 85.7%; Pred. No. 10;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GWLGPFD 8
|| ||||
Db 36 GWKGPFD 42

RESULT 7
JC5604
ABC-transporting peroxisomal membrane protein 69 - human
C;Species: Homo sapiens (man)
C;Date: 23-Sep-1997 #sequence_revision 23-Sep-1997 #text_change 02-Feb-2001
C;Accession: JC5604

GenCore version 5.1.4_p5_4578

OM protein - protein search, using sw model

Run on: April 16, 2003, 16:57:42 ; Search time 1.76842 Seconds
(without alignments)
211.085 Million cell updates/sec

Title: US-09-644-668A-37
Perfect score: 58
Sequence: 1 TGWLGPFDY 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	43	74.1	365	1	FCGN_MOUSE	Q61559 mus musculu
2	42	72.4	970	1	Y277_MYCGE	Q49409 mycoplasma
3	41	70.7	499	1	OPS1_PATYE	O15973 patinopecte
4	39.5	68.1	606	1	ABD4_HUMAN	O14678 homo sapien
5	39.5	68.1	606	1	ABD4_MOUSE	O89016 mus musculu
6	39	67.2	365	1	FCGN_HUMAN	P55899 homo sapien
7	39	67.2	401	1	HISZ_SYNY3	P74592 synechocyst
8	39	67.2	971	1	Y277_MYCPN	P75387 mycoplasma
9	38	65.5	143	1	GSPG_XANCP	P31734 xanthomonas
10	38	65.5	344	1	NU1M_CYACA	P48899 cyanidium c
11	37	63.8	118	1	GHRL_PIG	Q9gky5 sus scrofa
12	37	63.8	400	1	YHIN_ECOLI	P37631 escherichia
13	37	63.8	401	1	YHIN_HAEIN	P44941 haemophilus
14	37	63.8	430	1	SHU2_ECOLI	P09746 escherichia
15	36	62.1	304	1	HEMZ_THEVO	Q978u9 thermoplasm
16	36	62.1	308	1	HEMZ_THEAC	Q9hlb8 thermoplasm
17	36	62.1	343	1	HMAA_TRICA	Q07961 tribolium c
18	36	62.1	542	1	GUAA_SYNY3	P49057 synechocyst
19	36	62.1	566	1	PRIM_BPT3	P20315 bacteriopha
20	36	62.1	566	1	PRIM_BPT7	P03692 bacteriopha
21	36	62.1	694	1	LCF4_YEAST	P47912 saccharomyc
22	35.5	61.2	403	1	Y411_ARATH	O49562 arabidopsis
23	35	60.3	108	1	MAVI_CUCPE	P80728 cucurbita p
24	35	60.3	269	1	EXOK_RHIME	P33693 rhizobium m
25	35	60.3	318	1	MPD1_YEAST	Q12404 saccharomyc
26	35	60.3	322	1	NUOH_BUCAI	P57258 buchnera ap
27	35	60.3	366	1	FCGN_RAT	P13599 rattus norv
28	35	60.3	431	1	ORDL_HAEIN	P44732 haemophilus
29	35	60.3	433	1	GAG_HTLV2	P03346 human t-cel
30	35	60.3	478	1	RECQ_SYNY3	P73421 synechocyst
31	35	60.3	551	1	COX1_SYNY3	Q06473 synechocyst
32	34	58.6	174	1	IHBB_RAT	P17491 rattus norv
33	34	58.6	212	1	YQ15_CAEEL	Q09230 caenorhabdi
34	34	58.6	256	1	CB2_CHLMO	P22686 chlamydomon
35	34	58.6	259	1	RFBD_YEREN	Q56902 yersinia en
36	34	58.6	260	1	YFAX_ECOLI	P77732 escherichia
37	34	58.6	286	1	CYSW_SYNP7	P27370 synechococc
38	34	58.6	307	1	SYPH_BOVIN	P20488 bos taurus
39	34	58.6	307	1	SYPH_RAT	P07825 rattus norv
40	34	58.6	308	1	SYPH_MOUSE	Q62277 mus musculu
41	34	58.6	313	1	SYPH_HUMAN	P08247 homo sapien
42	34	58.6	375	1	MCK1_YEAST	P21965 saccharomyc
43	34	58.6	391	1	NUCC_MESVI	Q9mul0 mesostigma
44	34	58.6	392	1	NUCC_MARPO	P12131 marchantia
45	34	58.6	393	1	NUCC_ARATH	P56753 arabidopsis

ALIGNMENTS

RESULT 1
FCGN_MOUSE
ID FCGN_MOUSE STANDARD; PRT; 365 AA.
AC Q61559;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE IGG receptor FCRN large subunit P51 precursor (FCRN) (Neonatal FC
DE receptor) (IGG FC fragment receptor transporter, alpha chain).
GN FCGRT OR FCRN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Small intestine;
RX MEDLINE=95270984; PubMed=7538537;
RA Kandil E., Noguchi M., Ishibashi T., Kasahara M.;
RT "Structural and phylogenetic analysis of the MHC class I-like Fc
RT receptor gene.";
RL J. Immunol. 154:5907-5918(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Small intestine;
RX MEDLINE=94065162; PubMed=7504013;
RA Ahouse J.J., Hagerman C.L., Mittal P., Gilbert D.J.,
RA Copeland N.G., Jenkins N.A., Simister N.E.;
RT "Mouse MHC class I-like Fc receptor encoded outside the MHC.";
RL J. Immunol. 151:6076-6088(1993).
CC -!- FUNCTION: BINDS TO THE FC REGION OF MONOMERIC IMMUNOGLOBULINS
CC GAMMA. MEDIATES THE SELECTIVE UPTAKE OF IGG FROM MILK AND HELPS
CC NEWBORN ANIMALS TO ACQUIRE PASSIVE IMMUNITY. IGG IN THE MILK IS
CC BOUND AT THE APICAL SURFACE OF THE INTESTINAL EPITHELIUM. THE
CC RESULTANT FCRN-IGG COMPLEXES ARE TRANSCYTOSED ACROSS THE
CC INTESTINAL EPITHELIUM AND IGG IS RELEASED FROM FCRN INTO BLOOD OR
CC TISSUE FLUIDS.
CC -!- SUBUNIT: FCRN COMPLEX CONSIST OF TWO SUBUNITS: P51, AND P14 WHICH
CC IS EQUIVALENT TO BETA-2-MICROGLOBULIN. IT FORMS AN MCH CLASS I-
CC LIKE HETERODIMER.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: INTESTINAL EPITHELIUM OF SUKCLING RODENTS.
CC EXPRESSED IN NEONATAL INTESTINE AND FETAL YOLK SAC.
CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC ---

CC ---
DR EMBL; D37874; BAA07111.1; -.
DR EMBL; D37873; BAA07110.1; -.
DR EMBL; D37872; BAA07110.1; JOINED.

```
DR   EMBL; L17022; AAA16904.1; -.
DR   HSSP; P13599; 3FRU.
DR   MGD; MGI:103017; Fcgrt.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR001039; MHC_I.
DR   Pfam; PF00047; ig; 1.
DR   Pfam; PF00129; MHC_I; 1.
DR   ProDom; PD000050; MHC_I; 1.
DR   SMART; SM00407; IGc1; 1.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   IgG-binding protein; Receptor; Transmembrane; Glycoprotein; Signal;
KW   Immunoglobulin domain; Polymorphism.
FT   SIGNAL        1     21       BY SIMILARITY.
FT   CHAIN        22    365       IGG RECEPTOR FCRN LARGE SUBUNIT P51.
FT   DOMAIN       22    110       EXTRACELLULAR ALPHA-1.
FT   DOMAIN      111    200       EXTRACELLULAR ALPHA-2.
FT   DOMAIN      201    290       EXTRACELLULAR ALPHA-3.
FT   DOMAIN      291    297       CONNECTING PEPTIDE.
FT   TRANSMEM    298    321       POTENTIAL.
FT   DOMAIN      322    365       CYTOPLASMIC (POTENTIAL).
FT   DISULFID    119    182       BY SIMILARITY.
FT   DISULFID    221    275       BY SIMILARITY.
FT   CARBOHYD    108    108       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    125    125       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    149    149       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    246    246       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARIANT      73     73       M -> V (IN STRAIN FVB/N).
FT   VARIANT     111    111       Y -> F (IN STRAIN P/J).
SQ   SEQUENCE   365 AA;  40092 MW;  0A2290A54507E0C4 CRC64;

  Query Match             74.1%;  Score 43;  DB 1;  Length 365;
  Best Local Similarity   77.8%;  Pred. No. 2.7;
  Matches    7;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 TGWLGPFDY 9
           ||||||  |
Db      48 TGWLGPQQY 56


RESULT 2
Y277_MYCGE
ID   Y277_MYCGE     STANDARD;      PRT;   970 AA.
AC   Q49409; Q49253;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Hypothetical protein MG277.
GN   MG277.
OS   Mycoplasma genitalium.
OC   Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX   NCBI_TaxID=2097;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ATCC 33530 / G-37;
RX   MEDLINE=96026346; PubMed=7569993;
RA   Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A.,
RA   Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M.,
RA   Fritchman J.L., Weidman J.F., Small K.V., Sandusky M., Fuhrmann J.L.,
RA   Nguyen D.T., Utterback T.R., Saudek D.M., Phillips C.A., Merrick J.M.,
RA   Tomb J.-F., Dougherty B.A., Bott K.F., Hu P.-C., Lucier T.S.,
RA   Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.;
RT   "The minimal gene complement of Mycoplasma genitalium.";
RL   Science 270:397-403(1995).
RN   [2]
RP   SEQUENCE OF 624-678 FROM N.A.
RC   STRAIN=ATCC 33530 / G-37;
RX   MEDLINE=94075230; PubMed=8253680;
RA   Peterson S.N., Hu P.-C., Bott K.F., Hutchison C.A. III;
RT   "A survey of the Mycoplasma genitalium genome by using random
RT   sequencing.";
RL   J. Bacteriol. 175:7918-7930(1993).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U39707; AAC71499.1; -.
DR   EMBL; U02116; AAD12390.1; -.
DR   TIGR; MG277; -.
KW   Hypothetical protein; Transmembrane; Complete proteome.
FT   TRANSMEM     11     31       POTENTIAL.
FT   TRANSMEM    515    535       POTENTIAL.
FT   TRANSMEM    537    557       POTENTIAL.
FT   TRANSMEM    558    578       POTENTIAL.
FT   TRANSMEM    614    634       POTENTIAL.
FT   TRANSMEM    645    665       POTENTIAL.
FT   TRANSMEM    726    746       POTENTIAL.
FT   TRANSMEM    762    782       POTENTIAL.
FT   TRANSMEM    789    809       POTENTIAL.
FT   TRANSMEM    816    836       POTENTIAL.
FT   TRANSMEM    877    897       POTENTIAL.
FT   TRANSMEM    903    923       POTENTIAL.
FT   DOMAIN       50     53       POLY-THR.
FT   DOMAIN      370    382       POLY-ASN.
FT   CONFLICT    673    678       SGANWK -> QVQMKA (IN REF. 2).
SQ   SEQUENCE   970 AA;  108163 MW;  F106CDFCC9BD44FF CRC64;

  Query Match             72.4%;  Score 42;  DB 1;  Length 970;
  Best Local Similarity   75.0%;  Pred. No. 10;
  Matches    6;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2 GWLGPFDY 9
           ||| ||:|
Db     932 GWLSPFNY 939


RESULT 3
OPS1_PATYE
ID   OPS1_PATYE     STANDARD;      PRT;   499 AA.
AC   O15973;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   Rhodopsin, GQ-coupled (GQ-rhodopsin).
GN   SCOP1.
OS   Patinopecten yessoensis (Ezo giant scallop) (Yesso scallop).
OC   Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorphia; Pectinoida;
OC   Pectinoidea; Pectinidae; Mizuhopecten.
OX   NCBI_TaxID=6573;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Eye;
RX   MEDLINE=97435252; PubMed=9287291;
RA   Kojima D., Terakita A., Ishikawa T., Tsukahara Y., Maeda A.,
RA   Shichida Y.;
RT   "A novel Go-mediated phototransduction cascade in scallop visual
RT   cells.";
RL   J. Biol. Chem. 272:22979-22989(1997).
CC   -!- FUNCTION: VISUAL PIGMENTS ARE THE LIGHT-ABSORBING MOLECULES THAT
CC       MEDIATE VISION. THEY CONSIST OF AN APOPROTEIN, OPSIN, COVALENTLY
CC       LINKED TO CIS-RETINAL.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- TISSUE SPECIFICITY: RETINA. EXPRESSED IN THE DEPOLARIZING CELL
CC       LAYER OF THE PHOTORECPTOR CELLS DISTANT FROM THE LENS.
CC   -!- PTM: SOME OR ALL OF THE CARBOXYL-TERMINAL SER OR THR RESIDUES MAY
CC       BE PHOSPHORYLATED (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC       OPSIN SUBFAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
```

GenCore version 5.1.4_p5_4578

OM protein - protein search, using sw model

Run on: April 16, 2003, 17:13:59 ; Search time 9.22105 Seconds
(without alignments)
201.108 Million cell updates/sec

Title: US-09-644-668A-37
Perfect score: 58
Sequence: 1 TGWLGPFDY 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Tot number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_21:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

red. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	43	74.1	177	11	Q9R2A5	Q9r2a5 mus musculu
2	43	74.1	177	11	Q9QUR0	Q9qur0 mus musculu
3	41	70.7	286	2	O30544	O30544 agrobacteri
4	41	70.7	286	2	Q9R6D6	Q9r6d6 agrobacteri
5	41	70.7	286	16	Q8U604	Q8u604 agrobacteri
6	41	70.7	298	2	O69061	O69061 pseudomonas
7	41	70.7	328	8	Q37629	Q37629 prototheca
8	41	70.7	347	16	Q98KR3	Q98kr3 rhizobium l
9	40	69.0	214	16	Q8YDP6	Q8ydp6 brucella me
10	39.5	68.1	606	4	Q96E75	Q96e75 homo sapien
11	39	67.2	81	4	O75996	O75996 homo sapien
12	39	67.2	212	4	Q9NTW3	Q9ntw3 homo sapien
13	39	67.2	250	13	Q9W6R7	Q9w6r7 fugu rubrip
14	39	67.2	251	10	Q941Y2	Q941y2 oryza sativ
15	39	67.2	269	10	Q94E27	Q94e27 oryza sativ
16	39	67.2	273	9	Q9MCP8	Q9mcp8 bacteriopha
17	39	67.2	335	2	Q9KGW2	Q9kgw2 pseudomonas
18	39	67.2	362	4	Q9HBV7	Q9hbv7 homo sapien
19	39	67.2	365	4	Q9NZ19	Q9nz19 homo sapien
20	39	67.2	365	6	Q8SPV9	Q8spv9 macaca fasc
21	39	67.2	401	16	Q9RY03	Q9ry03 deinococcus
22	39	67.2	487	10	Q93Z90	Q93z90 arabidopsis
23	39	67.2	577	4	Q9UKM5	Q9ukm5 homo sapien
24	39	67.2	591	4	Q9UKM6	Q9ukm6 homo sapien
25	39	67.2	599	4	Q8WU48	Q8wu48 homo sapien
26	39	67.2	646	10	Q9STV1	Q9stv1 arabidopsis
27	39	67.2	660	4	Q96GD3	Q96gd3 homo sapien
28	39	67.2	664	11	Q9JME0	Q9jme0 mus musculu
29	39	67.2	700	4	Q9UQR0	Q9uqr0 homo sapien
30	39	67.2	719	16	Q8XWU4	Q8xwu4 ralstonia s
31	39	67.2	722	11	Q99MW4	Q99mw4 mus musculu
32	39	67.2	877	5	Q24191	Q24191 drosophila
33	39	67.2	877	5	Q9VHA0	Q9vha0 drosophila
34	37	63.8	168	16	Q8XVV3	Q8xvv3 ralstonia s
35	37	63.8	170	10	Q43076	Q43076 avena sativ
36	37	63.8	198	12	Q9QCC7	Q9qcc7 hepatitis c
37	37	63.8	365	2	O30835	O30835 rhodobacter
38	37	63.8	377	16	Q8YI31	Q8yi31 brucella me
39	37	63.8	393	16	Q9A886	Q9a886 caulobacter
40	37	63.8	394	16	Q92RY0	Q92ry0 rhizobium m
41	37	63.8	398	16	Q9KVQ9	Q9kvq9 vibrio chol
42	37	63.8	398	16	Q8ZLD8	Q8zld8 salmonella
43	37	63.8	398	16	Q8ZA52	Q8za52 yersinia pe
44	37	63.8	400	16	Q8Z267	Q8z267 salmonella
45	37	63.8	400	16	Q8X5R3	Q8x5r3 escherichia

ALIGNMENTS

RESULT 1
Q9R2A5
ID Q9R2A5 PRELIMINARY; PRT; 177 AA.
AC Q9R2A5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Fc receptor FcRn (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=P/J;
RX MEDLINE=95270984; PubMed=7538537;
RA Kandil E., Noguchi M., Ishibashi T., Kasahara M.;
RT "Structural and phylogenetic analysis of the MHC class I-like Fc
RT receptor gene1.";
RL J. Immunol. 154:5907-5918(1995).
DR EMBL; D37909; BAA07137.1; -.
DR EMBL; D37908; BAA07137.1; JOINED.
DR HSSP; P13599; 3FRU.
DR InterPro; IPR001039; MHC_I.
DR Pfam; PF00129; MHC_I; 1.
DR PRINTS; PR01638; MHCCLASSI.
DR ProDom; PD000050; MHC_I; 1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 177 177
SQ SEQUENCE 177 AA; 20369 MW; 2290C5EE49393CBD CRC64;

Query Match 74.1%; Score 43; DB 11; Length 177;
Best Local Similarity 77.8%; Pred. No. 6.5;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy       1 TGWLGPFDY 9
           ||||||  |
Db      25 TGWLGPQQY 33
```

```
RESULT 2
Q9QUR0
ID   Q9QUR0      PRELIMINARY;      PRT;   177 AA.
AC   Q9QUR0;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   FC receptor FcRn (Fragment).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=TW75, C3H, AKR, DBA/2, AND A/J;
RX   MEDLINE=95270984; PubMed=7538537;
RA   Kandil E., Noguchi M., Ishibashi T., Kasahara M.;
RT   "Structural and phylogenetic analysis of the MHC class I-like Fc
RT   receptor gene.";
RL   J. Immunol. 154:5907-5918(1995).
DR   EMBL; D37913; BAA07139.1; -.
DR   EMBL; D37912; BAA07139.1; JOINED.
DR   EMBL; D37903; BAA07134.1; -.
DR   EMBL; D37902; BAA07134.1; JOINED.
DR   EMBL; D37905; BAA07135.1; -.
DR   EMBL; D37904; BAA07135.1; JOINED.
DR   EMBL; D37907; BAA07136.1; -.
DR   EMBL; D37906; BAA07136.1; JOINED.
DR   EMBL; D37911; BAA07138.1; -.
DR   EMBL; D37910; BAA07138.1; JOINED.
DR   HSSP; P13599; 3FRU.
DR   InterPro; IPR001039; MHC_I.
DR   Pfam; PF00129; MHC_I; 1.
DR   PRINTS; PR01638; MHCCLASSI.
DR   ProDom; PD000050; MHC_I; 1.
KW   Receptor.
FT   NON_TER       1     1
FT   NON_TER     177   177
SQ   SEQUENCE   177 AA;  20385 MW;  228E2AF0B8D62252 CRC64;

  Query Match             74.1%;  Score 43;  DB 11;  Length 177;
  Best Local Similarity   77.8%;  Pred. No. 6.5;
  Matches    7;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 TGWLGPFDY 9
           |||||  |
Db      25 TGWLGPQQY 33


RESULT 3
O30544
ID   O30544      PRELIMINARY;      PRT;   286 AA.
AC   O30544;
DT   01-JAN-1998 (TrEMBLrel. 05, Created)
DT   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   AccE.
GN   ACCE.
OS   Agrobacterium tumefaciens (strain C58 / ATCC 33970).
OG   Plasmid pTiC58.
OC   Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC   Rhizobiaceae; Rhizobium.
OX   NCBI_TaxID=176299;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C58;
RX   MEDLINE=95113783; PubMed=7814335;
RA   Hwang I., Cook D.M., Farrand S.K.;
RT   "A new regulatory element modulates homoserine lactone-mediated
RT   autoinduction of Ti plasmid conjugal transfer.";
RL   J. Bacteriol. 177:449-458(1995).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C58;
RX   MEDLINE=96312367; PubMed=8763953;
RA   Farrand S.K., Hwang I., Cook D.M.;
RT   "The tra region of the nopaline-type Ti plasmid is a chimera with
RT   elements related to the transfer systems of RSF1010, RP4, and F.";
RL   J. Bacteriol. 178:4233-4247(1996).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C58;
RX   MEDLINE=98053873; PubMed=9393724;
RA   Kim H., Farrand S.K.;
RT   "Characterization of the acc operon from the nopaline-type Ti plasmid
RT   pTiC58, which encodes utilization of agrocinopines A and B and
RT   susceptibility to agrocin 84.";
RL   J. Bacteriol. 179:7559-7572(1997).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C58;
RA   Kim H., Farrand S.K.;
RL   Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C58;
RA   Piper K.R., Beck von Bodman S., Cook D.M., Hwang I., Kim H.,
RA   Farrand S.K.;
RL   Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF010180; AAC17201.1; -.
DR   InterPro; IPR000515; BPD_transp.
DR   Pfam; PF00528; BPD_transp; 1.
DR   PROSITE; PS00402; BPD_TRANSP_INN_MEMBR; UNKNOWN_1.
KW   Plasmid.
SQ   SEQUENCE   286 AA;  31025 MW;  1DBA970800F08C70 CRC64;

  Query Match             70.7%;  Score 41;  DB 2;  Length 286;
  Best Local Similarity   85.7%;  Pred. No. 24;
  Matches    6;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3 WLGPFDY 9
           || ||||
Db      43 WLAPFDY 49


RESULT 4
Q9R6D6
ID   Q9R6D6      PRELIMINARY;      PRT;   286 AA.
AC   Q9R6D6;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   TIORF124 protein.
GN   TIORF124.
OS   Agrobacterium tumefaciens.
OG   Plasmid pTi-SAKURA.
OC   Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC   Rhizobiaceae; Rhizobium.
OX   NCBI_TaxID=358;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=MAFF301001;
RX   MEDLINE=20184752; PubMed=10721727;
RA   Suzuki K., Hattori Y., Uraji M., Ohta N., Iwata K., Murata K.,
RA   Katoh A., Yoshida K.;
RT   "Complete nucleotide sequence of a plant tumor-inducing Ti plasmid.";
RL   Gene 242:331-336(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=MAFF301001;
RX   MEDLINE=98193120; PubMed=9524202;
RA   Suzuki K., Ohta N., Hattori Y., Uraji M., Katoh A., Yoshida K.;
RT   "Novel structural difference between nopaline- and octopine- type trbJ
RT   gene:construction of genetic and physical map and sequencing of
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GenCore version 5.1.4_p5_4578

OM protein - protein search, using sw model

Run on: April 16, 2003, 16:56:17 ; Search time 7.13684 Seconds
(without alignments)
168.037 Million cell updates/sec

Title: US-09-644-668A-37
Perfect score: 58
Sequence: 1 TGWLGPFDY 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

To number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_101002:*
1: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
2: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
3: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:*
4: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:*
5: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1984.DAT:*
6: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1985.DAT:*
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11: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1990.DAT:*
12: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1991.DAT:*
13: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1992.DAT:*
14: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1993.DAT:*
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19: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1998.DAT:*
20: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1999.DAT:*
21: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA2000.DAT:*
22: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:*
23: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	58	100.0	9	22	AAB67492	Human heavy chain
2	58	100.0	9	22	AAB67497	Human heavy chain
3	58	100.0	118	22	AAB67508	Light chain variab
4	58	100.0	118	22	AAB67509	Light chain variab
5	58	100.0	118	22	AAB67513	Heavy chain variab
6	58	100.0	118	22	AAB67514	Heavy chain variab
7	46	79.3	599	22	AAY72375	Amphiphilic recomb
8	40	69.0	163	21	AAY93725	The heavy chain of
9	39.5	68.1	41	22	ABB28612	Peptide #1263 enco
10	39.5	68.1	41	22	ABB33795	Peptide #1301 enco
11	39.5	68.1	41	22	ABB19238	Protein #1237 enco
12	39.5	68.1	41	22	AAM54561	Human brain expres
13	39.5	68.1	41	22	AAM66968	Human bone marrow
14	39.5	68.1	41	22	AAM14828	Peptide #1262 enco
15	39.5	68.1	41	22	AAM27255	Peptide #1292 enco
16	39.5	68.1	41	22	AAM02553	Peptide #1235 enco
17	39.5	68.1	41	23	ABG36625	Human peptide enco
18	39	67.2	61	20	AAY11877	Human 5' EST secre
19	39	67.2	67	22	ABB31004	Peptide #3655 enco
20	39	67.2	67	22	ABB21572	Protein #3571 enco
21	39	67.2	67	22	AAM17193	Peptide #3627 enco
22	39	67.2	79	20	AAY11647	Human 5' EST secre
23	39	67.2	100	23	ABB78659	Human scml2 transc
24	39	67.2	354	22	AAB82604	Cattle IgG transpo
25	39	67.2	354	22	AAB82606	Sheep IgG transpor
26	39	67.2	383	21	AAB38442	Fragment of human
27	39	67.2	577	18	AAW37398	Human sex comb on
28	39	67.2	577	18	AAW37394	Human sex comb on
29	39	67.2	577	20	AAY18288	Human Scm protein
30	39	67.2	591	18	AAW37399	Human sex comb on
31	39	67.2	591	18	AAW37395	Human sex comb on
32	39	67.2	591	20	AAY18289	Human Scm protein
33	39	67.2	620	18	AAW37397	Human sex comb on
34	39	67.2	620	18	AAW37393	Human sex comb on
35	39	67.2	620	20	AAY18287	Human Scm protein
36	39	67.2	623	22	ABG03903	Novel human diagno
37	39	67.2	648	22	AAB94447	Human protein sequ
38	39	67.2	664	18	AAW37400	Mouse sex comb on
39	39	67.2	664	18	AAW37396	Mouse sex comb on
40	39	67.2	664	20	AAY18290	Mouse Scm protein
41	39	67.2	730	22	ABG28448	Novel human diagno
42	39	67.2	827	22	AAU07864	Polypeptide sequen
43	39	67.2	877	22	ABB64464	Drosophila melanog
44	38	65.5	54	22	AAU53935	Propionibacterium
45	38	65.5	110	21	AAB14306	Human secreted pro

ALIGNMENTS

RESULT 1
AAB67492
ID AAB67492 standard; peptide; 9 AA.
XX
AC AAB67492;
XX
DT 29-MAY-2001 (first entry)
XX
DE Human heavy chain complementarity determining region 3 (CDR3).
XX
KW Complementarity determining region; CDR; immune response; antibody;
KW cytotoxic T lymphocyte associated antigen-4; CTLA-4; B7 ligand; cancer;
KW autoimmune disease; infectious disease; inflammation; allergy;
KW rheumatoid arthritis; myasthenia gravis; lupus erythematosus;
KW multiple sclerosis; insulin-dependent diabetes mellitus; inflammation;
KW transplant rejection; graft versus host disease.
XX
OS Homo sapiens.
XX
PN WO200114424-A2.
XX
PD 01-MAR-2001.
XX
PF 24-AUG-2000; 2000WO-US23356.
XX
PR 24-AUG-1999; 99US-0150452.
XX
PA (MEDA-) MEDAREX INC.
XX
PI Korman AJ, Halk EL, Lonberg N;
XX
DR WPI; 2001-202933/20.
XX

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PD   01-MAR-2001.
XX
PF   24-AUG-2000; 2000WO-US23356.
XX
PR   24-AUG-1999;   99US-0150452.
XX
PA   (MEDA-) MEDAREX INC.
XX
PI   Korman AJ,  Halk EL,  Lonberg N;
XX
DR   WPI; 2001-202933/20.
XX
PT   Novel human sequence antibody that binds to human cytotoxic T
PT   lymphocyte associated antigen-4, useful for inducing, augmenting or
PT   prolonging immune response to antigen or for suppressing immune
PT   response in patient  -
XX
PS   Claim 25; Fig 8; 127pp; English.
XX
CC   The present sequence represents the heavy chain variable region of
CC   human antibody 10D1. This antibody specifically binds to human
CC   cytotoxic T lymphocyte associated antigen-4 (CTLA-4). Such antibodies
CC   are used in methods for inducing, augmenting or prolonging an immune
CC   response to an antigen in a patient, where the antibodies block
CC   binding of human CTLA-4 to human B7 ligands. The antibodies are
CC   also useful for treating autoimmune disease in a subject caused or
CC   exacerbated by increased activity of T cells and for treating prostate
CC   cancer, melanoma or epithelial cancer. A polyvalent or polyclonal
CC   antibody preparation comprising two antibodies of the invention are
CC   useful for suppressing a immune response in a patient. They are used for
CC   treating cancer, infectious diseases and promoting beneficial autoimmune
CC   reactions for the treatment of diseases with inflammatory or allergic
CC   components. The polyvalent or polyclonal preparations are useful for
CC   treating autoimmune diseases such as rheumatoid arthritis, myasthenia
CC   gravis and lupus erythematosus, multiple sclerosis, insulin-dependent
CC   diabetes mellitus, transplant rejection, and inflammation, graft versus
CC   host disease.
XX
SQ   Sequence   118 AA;

  Query Match             100.0%;  Score 58;  DB 22;  Length 118;
  Best Local Similarity   100.0%;  Pred. No. 0.014;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 TGWLGPFDY 9
           |||||||||
Db      99 TGWLGPFDY 107


RESULT 6
AAB67514
ID   AAB67514 standard; peptide; 118 AA.
XX
AC   AAB67514;
XX
DT   29-MAY-2001  (first entry)
XX
DE   Heavy chain variable region of anti-CTLA-4 antibody 10D1.
XX
KW   Complementarity determining region; CDR; immune response; antibody;
KW   cytotoxic T lymphocyte associated antigen-4; CTLA-4; B7 ligand; cancer;
KW   autoimmune disease; infectious disease; inflammation; allergy;
KW   rheumatoid arthritis; myasthenia gravis; lupus erythematosus;
KW   multiple sclerosis; insulin-dependent diabetes mellitus; inflammation;
KW   transplant rejection; graft versus host disease.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Region          31..35
FT                   /note= "CDR1"
FT   Region          50..66
FT                   /note= "CDR2"
FT   Region          99..107
FT                   /note= "CDR3"
XX
PN   WO200114424-A2.
XX
PD   01-MAR-2001.
XX
PF   24-AUG-2000; 2000WO-US23356.
XX
PR   24-AUG-1999;   99US-0150452.
XX
PA   (MEDA-) MEDAREX INC.
XX
PI   Korman AJ,  Halk EL,  Lonberg N;
XX
DR   WPI; 2001-202933/20.
XX
PT   Novel human sequence antibody that binds to human cytotoxic T
PT   lymphocyte associated antigen-4, useful for inducing, augmenting or
PT   prolonging immune response to antigen or for suppressing immune
PT   response in patient  -
XX
PS   Claim 26; Fig 8; 127pp; English.
XX
CC   The present sequence represents the heavy chain variable region of
CC   human antibody 10D1. This antibody specifically binds to human
CC   cytotoxic T lymphocyte associated antigen-4 (CTLA-4). Such antibodies
CC   are used in methods for inducing, augmenting or prolonging an immune
CC   response to an antigen in a patient, where the antibodies block
CC   binding of human CTLA-4 to human B7 ligands. The antibodies are
CC   also useful for treating autoimmune disease in a subject caused or
CC   exacerbated by increased activity of T cells and for treating prostate
CC   cancer, melanoma or epithelial cancer. A polyvalent or polyclonal
CC   antibody preparation comprising two antibodies of the invention are
CC   useful for suppressing a immune response in a patient. They are used for
CC   treating cancer, infectious diseases and promoting beneficial autoimmune
CC   reactions for the treatment of diseases with inflammatory or allergic
CC   components. The polyvalent or polyclonal preparations are useful for
CC   treating autoimmune diseases such as rheumatoid arthritis, myasthenia
CC   gravis and lupus erythematosus, multiple sclerosis, insulin-dependent
CC   diabetes mellitus, transplant rejection, and inflammation, graft versus
CC   host disease.
XX
SQ   Sequence   118 AA;

  Query Match             100.0%;  Score 58;  DB 22;  Length 118;
  Best Local Similarity   100.0%;  Pred. No. 0.014;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 TGWLGPFDY 9
           |||||||||
Db      99 TGWLGPFDY 107


RESULT 7
AAY72375
ID   AAY72375 standard; Protein; 599 AA.
XX
AC   AAY72375;
XX
DT   24-APR-2001  (first entry)
XX
DE   Amphiphilic recombinant collagen-like polymer, N1N2P4.
XX
KW   Recombinant protein; collagen-like polymer; gelatin-like polymer; N1N2P4;
KW   stabiliser; oil-in-water emulsion; foodstuff; pharmaceutical product;
KW   cosmetic product; photography.
XX
OS   Synthetic.
XX
PN   EP1063565-A1.
XX
PD   27-DEC-2000.
```

XX
PF 23-JUN-2000; 2000EP-0202206.
XX
PR 24-JUN-1999; 99EP-0202047.
XX
PA (FUJF) FUJI PHOTO FILM BV.
XX
PI Olijve JH, Bouwstra JB, De Wolf FA, Werten MWT, Wisselink HW;
PI Wind RD, Van Den Bosch TJ, Toda Y;
XX
DR WPI; 2001-125578/14.
XX
PT Oil-in-water emulsions for preparing foodstuffs, pharmaceutical product
PT or cosmetic product, comprises recombinant collagen-like polymer as
PT stabilizer -
XX
PS Example 6; Page 24-26; 31pp; English.
XX
CC The present sequence is a synthetic amphiphilic recombinant collagen-
CC like (or gelatin-like) polymer, N1N2P4 which contains two different
CC non-polar modules (N1) and four polar modules (P4). The N2 module
CC is similar to the N1 module, but differs mainly in the presence of
CC a cluster of methionine and charged residues at its C-terminal side.
CC This polymer exhibits an amphiphillic structure and is used as a
CC stabiliser for oil-in-water emulsions. The oil-in-water emulsion is
CC used for producing foodstuffs, pharmaceutical products or cosmetic
CC products by combining with nutritionally, pharmaceutically, and
CC cosmetically suitable ingredients. It is also useful in photography.
XX
SQ Sequence 599 AA;

Query Match 79.3%; Score 46; DB 22; Length 599;
Best Local Similarity 87.5%; Pred. No. 9.5;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GWLGPFDY 9
||||||:|
Db 142 GWLGPFGY 149

RESULT 8
AAY93725
ID AAY93725 standard; Protein; 163 AA.
XX
AC AAY93725;
XX
DT 03-OCT-2000 (first entry)
XX
DE ie heavy chain of immunoglobulin clone 12.9.1.1.
XX
KW Cytotoxic T-lymphocyte antigen-4; CTLA-4; antibody; immune system;
KW hyperimmunity disorder; autoimmune disease; diabetes; graft rejection;
KW proliferative disorder; cancer; immunodeficient disorder.
XX
OS Homo sapiens.
XX
PN WO200037504-A2.
XX
PD 29-JUN-2000.
XX
PF 23-DEC-1999; 99WO-US30895.
XX
PR 23-DEC-1998; 98US-0113647.
XX
PA (PFIZ) PFIZER INC.
PA (ABGE-) ABGENIX INC.
XX
PI Hanson DC, Neveu MJ, Mueller EE, Hanke JH, Gilman SC, Davis CG;
PI Corvalan JR;
XX
DR WPI; 2000-442647/38.
DR N-PSDB; AAA46888.
XX
PT Novel antibodies capable of binding cytotoxic T-lymphocyte antigen
PT (CTLA)-4 containing specified heavy and light chain sequences, useful
PT for treating, e.g. immune disorders -
XX
PS Claim 2; Fig 1M; 157pp; English.
XX
CC The present sequence represents a heavy chain of an antibody of the
CC invention. The antibody is directed cytotoxic T-lymphocyte antigen
CC (CTLA)-4. Antibodies of the invention are composed of a heavy chain
CC variable region, comprising a modified contiguous sequence from a
CC FR1-FR3 sequence encoded by a human VH3-33 family gene. The
CC modifications are contained in CDR1, CDR2 and/or framework regions.
CC The antibodies may be used to inhibit CTLA-4 and down-regulate the
CC immune system to treat hyperimmunity disorders (e.g. autoimmune
CC disease, diabetes and graft rejection) and proliferative disorders
CC (e.g. cancer). CTLA-4 stimulatory agents may be used to up-regulate
CC immune system to up-regulate immunodeficient disorders.
XX
SQ Sequence 163 AA;

Query Match 69.0%; Score 40; DB 21; Length 163;
Best Local Similarity 66.7%; Pred. No. 26;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TGWLGPFDY 9
|||:|||:
Db 91 TGWYGGFDF 99

RESULT 9
ABB28612
ID ABB28612 standard; Peptide; 41 AA.
XX
AC ABB28612;
XX
DT 01-FEB-2002 (first entry)
XX
DE Peptide #1263 encoded by breast cell single exon nucleic acid probe.
XX
KW Human; microarray; single exon probe; gene expression; breast;
KW disease; cancer.
XX
OS Homo sapiens.
XX
PN WO200157271-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US00662.
XX
PR 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-496933/54.
XX
PT New spatially-addressable set of single exon nucleic acid probes,
PT useful for measuring gene expression in sample derived from human
PT breast, comprises number of single exon nucleic acid probes -
XX
PS Claim 27; SEQ ID NO 11580; 327pp + sequence listing; English.
XX
CC The invention relates to a spatially-addressable set of single exon
CC nucleic acid probes for measuring gene expression in a sample derived
CC from human breast and BT 474 cells. The method involves contacting

```
CC   the probes with a collection of detectably labelled nucleic acids
CC   derived from mRNA of human breast, and then measuring the label
CC   bound to each probe of the microarray. The probes are useful for
CC   verifying the expression of regions of genomic DNA predicted to
CC   encode proteins. They are useful for gene discovery, and for
CC   determining predisposition and/or prognosing breast disease. Gene
CC   expression analysis is useful for assessing the toxicity of chemical
CC   agents on cells. The microarray of this invention presents a far greater
CC   diversity of probes for measuring gene expression, with far less bias
CC   than expressed sequence tag microarrays. The method is suitable for
CC   rapid production of functional information from genomic sequence. The
CC   present sequence is a peptide encoded by a single exon nucleic acid
CC   probe of the invention.
CC   Note: The sequence data for this patent did not form part of the
CC   printed specification, but was obtained in electronic format directly
CC   from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence   41 AA;

  Query Match             68.1%;  Score 39.5;  DB 22;  Length 41;
  Best Local Similarity   66.7%;  Pred. No. 7.5;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    3;  Gaps    1;

Qy       1 TGWLGP---FDY 9
           ||||||   | |
Db       1 TGWLGPVSIFGY 12


RESULT 10
ABB33795
ID   ABB33795 standard; Peptide; 41 AA.
XX
AC   ABB33795;
XX
DT   04-FEB-2002  (first entry)
XX
DE   Peptide #1301 encoded by human foetal liver single exon probe.
XX
KW   Human; foetal liver; gene expression; single exon nucleic acid probe.
XX
OS   Homo sapiens.
XX
PN   WO200157277-A2.
XX
PD   09-AUG-2001.
XX
PF   30-JAN-2001; 2001WO-US00669.
XX
PR   04-FEB-2000; 2000US-0180312.
PR   26-MAY-2000; 2000US-0207456.
PR   30-JUN-2000; 2000US-0608408.
PR   03-AUG-2000; 2000US-0632366.
PR   21-SEP-2000; 2000US-0234687.
PR   27-SEP-2000; 2000US-0236359.
PR   04-OCT-2000; 2000GB-0024263.
XX
PA   (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI   Penn SG,  Hanzel DK,  Chen W,  Rank DR;
XX
DR   WPI; 2001-483447/52.
XX
PT   Human genome-derived single exon nucleic acid probes useful for
PT   analyzing gene expression in human fetal liver -
XX
PS   Claim 27; SEQ ID NO 26430; 639pp + sequence listing; English.
XX
CC   The invention relates to a single exon nucleic acid probe for
CC   measuring human gene expression in a sample derived from human foetal
CC   liver. The single exon nucleic acid probes may be used for predicting,
CC   measuring and displaying gene expression in samples derived from human
CC   fetal liver. The present sequence is a peptide encoded by a single exon
CC   nucleic acid probe of the invention.
CC   Note: The sequence data for this patent did not form part of the
CC   printed specification, but was obtained in electronic format directly
CC   from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence   41 AA;

  Query Match             68.1%;  Score 39.5;  DB 22;  Length 41;
  Best Local Similarity   66.7%;  Pred. No. 7.5;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    3;  Gaps    1;

Qy       1 TGWLGP---FDY 9
           ||||||   | |
Db       1 TGWLGPVSIFGY 12


RESULT 11
ABB19238
ID   ABB19238 standard; Protein; 41 AA.
XX
AC   ABB19238;
XX
DT   23-JAN-2002  (first entry)
XX
DE   Protein #1237 encoded by probe for measuring heart cell gene expression.
XX
KW   Human; gene expression; heart; microarray; vascular system;
KW   cardiovascular disease; hypertension; cardiac arrhythmia;
KW   congenital heart disease.
XX
OS   Homo sapiens.
XX
PN   WO200157274-A2.
XX
PD   09-AUG-2001.
XX
PF   30-JAN-2001; 2001WO-US00666.
XX
PR   04-FEB-2000; 2000US-0180312.
PR   26-MAY-2000; 2000US-0207456.
PR   30-JUN-2000; 2000US-0608408.
PR   03-AUG-2000; 2000US-0632366.
PR   21-SEP-2000; 2000US-0234687.
PR   27-SEP-2000; 2000US-0236359.
PR   04-OCT-2000; 2000GB-0024263.
XX
PA   (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI   Penn SG,  Hanzel DK,  Chen W,  Rank DR;
XX
DR   WPI; 2001-488899/53.
XX
PT   Single exon nucleic acid probes for analyzing gene expression in human
PT   hearts -
XX
PS   Claim 15; SEQ ID No 21008; 530pp; English.
XX
CC   The present invention relates to single exon nucleic acid probes for
CC   measuring human gene expression in a sample derived from human heart (see
CC   ABA21535-ABA41305). The present sequence is a protein encoded by one such
CC   probe. The probes may be used for predicting, measuring and displaying
CC   gene expression in samples derived from the human heart via microarrays.
CC   By measuring gene expression, the probes are useful for predicting,
CC   diagnosing, grading, staging, monitoring and prognosing diseases of the
CC   human heart and vascular system e.g. cardiovascular disease,
CC   hypertension, cardiac arrhythmias and congenital heart disease.
CC   Note: The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence   41 AA;

  Query Match             68.1%;  Score 39.5;  DB 22;  Length 41;
  Best Local Similarity   66.7%;  Pred. No. 7.5;
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OM protein - protein search, using sw model

Run on: April 16, 2003, 17:21:54 ; Search time 2.65263 Seconds
(without alignments)
256.547 Million cell updates/sec

Title: US-09-644-668A-37
Perfect score: 58
Sequence: 1 TGWLGPFDY 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 288829 seqs, 75613885 residues

To number of hits satisfying chosen parameters: 288829

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
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2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
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11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
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14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	42	72.4	408	9	US-10-140-372-3	Sequence 3, Appli
2	39.5	68.1	41	10	US-09-864-761-34536	Sequence 34536, A
3	39	67.2	67	10	US-09-864-761-36870	Sequence 36870, A
4	39	67.2	100	10	US-09-872-523-15	Sequence 15, Appl
5	39	67.2	383	9	US-10-050-704-239	Sequence 239, App
6	39	67.2	827	10	US-09-801-574-12	Sequence 12, Appl
7	38	65.5	110	10	US-09-740-668A-14	Sequence 14, Appl
8	38	65.5	110	10	US-09-915-582-70	Sequence 70, Appl
9	37	63.8	400	10	US-09-815-242-10380	Sequence 10380, A
10	37	63.8	401	10	US-09-815-242-11155	Sequence 11155, A
11	37	63.8	419	10	US-09-815-242-13798	Sequence 13798, A
12	35.5	61.2	436	9	US-09-738-626-3877	Sequence 3877, Ap
13	35	60.3	15	9	US-09-880-748-2958	Sequence 2958, Ap
14	35	60.3	117	10	US-09-861-451A-70	Sequence 70, Appl
15	35	60.3	154	10	US-09-925-301-1526	Sequence 1526, Ap
16	35	60.3	252	9	US-09-880-748-1201	Sequence 1201, Ap
17	35	60.3	252	9	US-09-880-748-1519	Sequence 1519, Ap
18	35	60.3	257	9	US-09-738-626-6656	Sequence 6656, Ap
19	35	60.3	431	10	US-09-815-242-11033	Sequence 11033, A
20	35	60.3	530	9	US-09-738-626-4188	Sequence 4188, Ap
21	35	60.3	1198	9	US-09-975-719-405	Sequence 405, App
22	34	58.6	68	9	US-09-796-692-1775	Sequence 1775, Ap
23	34	58.6	77	9	US-09-796-692-2255	Sequence 2255, Ap
24	34	58.6	77	9	US-09-796-692-2265	Sequence 2265, Ap
25	34	58.6	92	10	US-09-764-877-1874	Sequence 1874, Ap
26	34	58.6	141	10	US-09-073-009-15	Sequence 15, Appl
27	34	58.6	141	10	US-09-023-588-15	Sequence 15, Appl
28	34	58.6	141	10	US-09-793-306-15	Sequence 15, Appl
29	34	58.6	151	9	US-10-102-806-435	Sequence 435, App
30	34	58.6	307	10	US-09-036-613-7	Sequence 7, Appli
31	34	58.6	381	9	US-09-738-626-3549	Sequence 3549, Ap
32	34	58.6	400	10	US-09-073-009-126	Sequence 126, App
33	34	58.6	400	10	US-09-793-306-126	Sequence 126, App
34	34	58.6	408	9	US-09-813-398-20	Sequence 20, Appl
35	34	58.6	408	9	US-09-813-398-22	Sequence 22, Appl
36	34	58.6	412	9	US-09-978-295A-157	Sequence 157, App
37	34	58.6	412	9	US-09-978-697-157	Sequence 157, App
38	34	58.6	412	9	US-09-978-192A-157	Sequence 157, App
39	34	58.6	412	9	US-09-999-832A-157	Sequence 157, App
40	34	58.6	412	9	US-10-001-054-8	Sequence 8, Appli
41	34	58.6	412	9	US-09-978-189-157	Sequence 157, App
42	34	58.6	412	9	US-09-978-608A-157	Sequence 157, App
43	34	58.6	412	9	US-09-978-191A-157	Sequence 157, App
44	34	58.6	412	9	US-09-978-403A-157	Sequence 157, App
45	34	58.6	412	9	US-09-978-564A-157	Sequence 157, App

ALIGNMENTS

RESULT 1
US-10-140-372-3
; Sequence 3, Application US/10140372
; Publication No. US20030021789A1
; GENERAL INFORMATION:
; APPLICANT: XU, Yi
; APPLICANT: HOOK, Magnus A.O.
; TITLE OF INVENTION: SURFACE PROTEINS FROM GRAM-POSITIVE BACTERIA
; FILE REFERENCE: P07196US01/BAS
; CURRENT APPLICATION NUMBER: US/10/140,372
; CURRENT FILING DATE: 2002-05-08
; PRIOR APPLICATION NUMBER: US 60/289,132
; PRIOR FILING DATE: 2001-05-08
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 408
; TYPE: PRT
; ORGANISM: Streptococcus mutans
US-10-140-372-3

Query Match 72.4%; Score 42; DB 9; Length 408;
Best Local Similarity 66.7%; Pred. No. 23;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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Qy       1 TGWLGPFDY 9
           : || ||||
Db     239 SAWLNPFDY 247
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RESULT 2
US-09-864-761-34536
; Sequenoe 34536, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aeomica-X-1

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; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE:  2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
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; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
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;   LENGTH: 41
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: MAP TO AC005519.2
;   OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.1
;   OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.1
;   OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.98
;   OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 0.93
;   OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 0.99
;   OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.1
;   OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.3
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;   OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.3
;   OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL =   1
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;   OTHER INFORMATION: SWISSPROT HIT: O14678, EVALUE 1.00e-18
US-09-864-761-34536

  Query Match             68.1%;  Score 39.5;  DB 10;  Length 41;
  Best Local Similarity   66.7%;  Pred. No. 6.9;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    3;  Gaps    1;

Qy       1 TGWLGP---FDY 9
            ||||||   | |
Db       1 TGWLGPVSIFGY 12


RESULT 3
US-09-864-761-36870
; Sequence 36870, Application US/09864761
; Patent No. US20020048763A1
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```
; GENERAL INFORMATION:
;  APPLICANT: Penn, Sharron G.
;  APPLICANT:  Rank, David R.
;  APPLICANT:  Hanzel, David K.
;  APPLICANT:  Chen, Wensheng
;  TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
;  TITLE OF INVENTION:  GENE EXPRESSION ANALYSIS BY MICROARRAY
;  FILE REFERENCE: Aeomica-X-1
;  CURRENT APPLICATION NUMBER: US/09/864,761
;  CURRENT FILING DATE:  2001-05-23
;  PRIOR APPLICATION NUMBER: US 60/180,312
;  PRIOR FILING DATE: 2000-02-04
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: US 09/632,366
;  PRIOR FILING DATE: 2000-08-03
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00662
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00661
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00670
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 60/234,687
;  PRIOR FILING DATE: 2000-09-21
;  PRIOR APPLICATION NUMBER: US 09/608,408
;  PRIOR FILING DATE: 2000-06-30
;  PRIOR APPLICATION NUMBER: US 09/774,203
;  PRIOR FILING DATE: 2001-01-29
;  NUMBER OF SEQ ID NOS: 49117
;  SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 36870
;   LENGTH: 67
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: MAP TO AL110502.1
;   OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.93
;   OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.2
;   OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.1
;   OTHER INFORMATION: SWISSPROT HIT: Q01441, EVALUE 3.00e+00
;   OTHER INFORMATION: EST_HUMAN HIT: BE257700.1, EVALUE 4.00e-37
US-09-864-761-36870

  Query Match             67.2%;  Score 39;  DB 10;  Length 67;
  Best Local Similarity   75.0%;  Pred. No. 13;
  Matches    6;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2 GWLGPFDY 9
            || | |||
Db      32 GWRGAFDY 39


RESULT 4
US-09-872-523-15
; Sequence 15, Application US/09872523
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OM protein - protein search, using sw model

Run on: April 16, 2003, 17:15:40 ; Search time 2.30526 Seconds
(without alignments)
114.870 Million cell updates/sec

Title: US-09-644-668A-37
Perfect score: 58
Sequence: 1 TGWLGPFDY 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

To number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	39	67.2	577	2	US-08-852-153-4	Sequence 4, Appli
2	39	67.2	591	2	US-08-852-153-6	Sequence 6, Appli
	39	67.2	620	2	US-08-852-153-2	Sequence 2, Appli
	39	67.2	664	2	US-08-852-153-8	Sequence 8, Appli
5	36	62.1	12	2	US-08-406-330-33	Sequence 33, Appl
6	36	62.1	12	2	US-08-556-597-33	Sequence 33, Appl
7	35	60.3	121	1	US-08-339-582-2	Sequence 2, Appli
8	35	60.3	136	4	US-08-259-451-5	Sequence 5, Appli
9	35	60.3	366	1	US-08-004-492-8	Sequence 8, Appli
10	35	60.3	432	5	PCT-US95-04910-13	Sequence 13, Appl
11	35	60.3	433	1	US-07-672-483-4	Sequence 4, Appli
12	35	60.3	433	4	US-08-259-451-3	Sequence 3, Appli
13	35	60.3	1198	4	US-09-199-637A-405	Sequence 405, App
14	34	58.6	27	1	US-08-383-753-20	Sequence 20, Appl
15	34	58.6	27	2	US-08-586-772-20	Sequence 20, Appl
16	34	58.6	27	2	US-08-959-512-20	Sequence 20, Appl
17	34	58.6	27	4	US-09-512-983-20	Sequence 20, Appl
18	34	58.6	262	4	US-09-372-422A-32	Sequence 32, Appl
19	34	58.6	296	2	US-08-700-637-4	Sequence 4, Appli
20	34	58.6	307	1	US-07-982-112-2	Sequence 2, Appli
21	34	58.6	390	4	US-09-134-001C-3112	Sequence 3112, Ap
22	34	58.6	616	2	US-09-001-826-5	Sequence 5, Appli
23	34	58.6	621	3	US-08-604-789B-4	Sequence 4, Appli
24	34	58.6	621	4	US-09-312-721A-4	Sequence 4, Appli
25	34	58.6	2972	4	US-08-469-260A-387	Sequence 387, App
26	33	56.9	119	1	US-08-478-039-65	Sequence 65, Appl
27	33	56.9	119	1	US-08-476-349A-65	Sequence 65, Appl
28	33	56.9	126	4	US-09-240-274-10	Sequence 10, Appl
29	33	56.9	126	4	US-09-240-274-144	Sequence 144, App
30	33	56.9	126	4	US-09-240-274-150	Sequence 150, App
31	33	56.9	127	4	US-09-240-274-11	Sequence 11, Appl
32	33	56.9	413	2	US-08-846-762-15	Sequence 15, Appl
33	33	56.9	413	2	US-08-846-762-88	Sequence 88, Appl
34	33	56.9	491	2	US-09-001-826-23	Sequence 23, Appl
35	33	56.9	577	4	US-09-486-382B-2	Sequence 2, Appli
36	33	56.9	577	4	US-09-486-382B-13	Sequence 13, Appl
37	33	56.9	593	5	PCT-US93-07923-11	Sequence 11, Appl
38	33	56.9	595	3	US-08-604-789B-3	Sequence 3, Appli
39	33	56.9	595	4	US-09-312-721A-3	Sequence 3, Appli
40	33	56.9	604	3	US-08-604-789B-2	Sequence 2, Appli
41	33	56.9	604	3	US-08-604-789B-16	Sequence 16, Appl
42	33	56.9	604	4	US-09-312-721A-2	Sequence 2, Appli
43	33	56.9	604	4	US-09-312-721A-16	Sequence 16, Appl
44	33	56.9	606	4	US-09-486-382B-11	Sequence 11, Appl
45	33	56.9	755	5	PCT-US93-07923-3	Sequence 3, Appli

ALIGNMENTS

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RESULT 1
US-08-852-153-4
; Sequence 4, Application US/08852153
; Patent No. 5914266
; GENERAL INFORMATION:
;   APPLICANT: Randazzo, Filippo
;   TITLE OF INVENTION: Mammalian Sex Comb on Midleg Acts as a Tumor Suppressor
;   NUMBER OF SEQUENCES: 8
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Chiron Corporation
;     STREET: 4560 Horton Street
;     CITY: Emeryville
;     STATE: California
;     COUNTRY: U.S.A.
;     ZIP: 94608
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/852,153
;     FILING DATE:
;     CLASSIFICATION: 435
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Guth, Joseph H.
;     REGISTRATION NUMBER: 31,261
;     REFERENCE/DOCKET NUMBER: 1224.006
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (510) 923-3888
;     TELEFAX: (510) 655-3542
; INFORMATION FOR SEQ ID NO: 4:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 577 amino acids
;     TYPE: amino acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-08-852-153-4

  Query Match           67.2%;  Score 39;  DB 2;  Length 577;
  Best Local Similarity  75.0%;  Pred. No. 60;
  Matches    6;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2 GWLGPFDY 9
            || | |||
Db     142 GWRGAFDY 149


RESULT 2
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US-08-852-153-6
; Sequence 6, Application US/08852153
; Patent No. 5914266
; GENERAL INFORMATION:
;   APPLICANT:  Randazzo, Filippo
;   TITLE OF INVENTION:  Mammalian Sex Comb on Midleg Acts as a Tumor Suppressor
;   NUMBER OF SEQUENCES:  8
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  Chiron Corporation
;     STREET:  4560 Horton Street
;     CITY:  Emeryville
;     STATE:  California
;     COUNTRY:  U.S.A.
;     ZIP:  94608
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Floppy disk
;     COMPUTER:  IBM PC compatible
;     OPERATING SYSTEM:  PC-DOS/MS-DOS
;     SOFTWARE:  PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/08/852,153
;     FILING DATE:
;     CLASSIFICATION:  435
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  Guth, Joseph H.
;     REGISTRATION NUMBER:  31,261
;     REFERENCE/DOCKET NUMBER:  1224.006
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  (510) 923-3888
;     TELEFAX:  (510) 655-3542
; INFORMATION FOR SEQ ID NO:  6:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH:  591 amino acids
;     TYPE:  amino acid
;     STRANDEDNESS:  single
;     TOPOLOGY:  linear
;   MOLECULE TYPE:  protein
US-08-852-153-6

  Query Match             67.2%;  Score 39;  DB 2;  Length 591;
  Best Local Similarity   75.0%;  Pred. No. 62;
  Matches    6;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2 GWLGPFDY 9
            || | |||
Db     156 GWRGAFDY 163


RESULT 3
US-08-852-153-2
; Sequence 2, Application US/08852153
; Patent No. 5914266
; GENERAL INFORMATION:
;   APPLICANT:  Randazzo, Filippo
;   TITLE OF INVENTION:  Mammalian Sex Comb on Midleg Acts as a Tumor Suppressor
;   NUMBER OF SEQUENCES:  8
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  Chiron Corporation
;     STREET:  4560 Horton Street
;     CITY:  Emeryville
;     STATE:  California
;     COUNTRY:  U.S.A.
;     ZIP:  94608
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Floppy disk
;     COMPUTER:  IBM PC compatible
;     OPERATING SYSTEM:  PC-DOS/MS-DOS
;     SOFTWARE:  PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/08/852,153
;     FILING DATE:
;     CLASSIFICATION:  435
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  Guth, Joseph H.
;     REGISTRATION NUMBER:  31,261
;     REFERENCE/DOCKET NUMBER:  1224.006
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  (510) 923-3888
;     TELEFAX:  (510) 655-3542
; INFORMATION FOR SEQ ID NO:  2:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH:  620 amino acids
;     TYPE:  amino acid
;     STRANDEDNESS:  single
;     TOPOLOGY:  linear
;   MOLECULE TYPE:  protein
US-08-852-153-2

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  Matches    6;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2 GWLGPFDY 9
            || | |||
Db     185 GWRGAFDY 192


RESULT 4
US-08-852-153-8
; Sequence 8, Application US/08852153
; Patent No. 5914266
; GENERAL INFORMATION:
;   APPLICANT:  Randazzo, Filippo
;   TITLE OF INVENTION:  Mammalian Sex Comb on Midleg Acts as a Tumor Suppressor
;   NUMBER OF SEQUENCES:  8
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  Chiron Corporation
;     STREET:  4560 Horton Street
;     CITY:  Emeryville
;     STATE:  California
;     COUNTRY:  U.S.A.
;     ZIP:  94608
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Floppy disk
;     COMPUTER:  IBM PC compatible
;     OPERATING SYSTEM:  PC-DOS/MS-DOS
;     SOFTWARE:  PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/08/852,153
;     FILING DATE:
;     CLASSIFICATION:  435
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  Guth, Joseph H.
;     REGISTRATION NUMBER:  31,261
;     REFERENCE/DOCKET NUMBER:  1224.006
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  (510) 923-3888
;     TELEFAX:  (510) 655-3542
; INFORMATION FOR SEQ ID NO:  8:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH:  664 amino acids
;     TYPE:  amino acid
;     STRANDEDNESS:  single
;     TOPOLOGY:  linear
;   MOLECULE TYPE:  protein
US-08-852-153-8

  Query Match             67.2%;  Score 39;  DB 2;  Length 664;
  Best Local Similarity   75.0%;  Pred. No. 69;
  Matches    6;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2 GWLGPFDY 9
            || | |||
Db     203 GWRGAFDY 210
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